

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223966 Seq. ID LIB3165-060-Q1-K1-F11 Method BLASTX NCBI GI q3763916 BLAST score 331 E value 6.0e-31 Match length 126 % identity NCBI Description (AC004450) unknown protein [Arabidopsis thaliana] >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown protein [Arabidopsis thaliana] Seq. No. 223967 Seq. ID LIB3165-060-Q1-K1-F12 Method BLASTX NCBI GI q729668 BLAST score 242 E value 1.0e-20 Match length 55 % identity 84 NCBI Description HISTONE H1 >gi\_2147479\_pir\_\_\$65059 histone H1, drought-inducible - Lycopersicon pennellii >gi 436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii] Seq. No. 223968 Seq. ID LIB3165-060-Q1-K1-F3 Method BLASTX NCBI GI g1352821 BLAST score 352 E value 1.0e-33 Match length 67 % identity 100 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223969 Seq. ID LIB3165-060-Q1-K1-F5 Method BLASTX

NCBI GI q4455223 BLAST score 403 E value 2.0e-39 Match length 126 % identity

NCBI Description (AL035440) putative DNA binding protein [Arabidopsis

thalianal

Seq. No. 223970

Seq. ID LIB3165-060-Q1-K1-F6



```
Method
                   BLASTX
NCBI GI
                   g464775
BLAST score
                   447
E value
                   1.0e-44
Match length
                   89
% identity
                   92
                   SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__$39492
NCBI Description
                   superoxide dismutase - Para rubber tree >gi_348137 (L11707)
                   superoxide dismutase (manganese) [Hevea brasiliensis]
Seq. No.
                   223971
Seq. ID
                   LIB3165-060-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   q3549626
BLAST score
                   294
E value
                   1.0e-26
Match length
                   99
% identity
                   55
NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
Seq. No.
                   223972
Seq. ID
                   LIB3165-060-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   g289920
BLAST score
                   429
E value
                   1.0e-42
Match length
                   82
% identity
                   98
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                   hirsutum]
Seq. No.
                   223973
Seq. ID
                   LIB3165-060-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   g1352821
BLAST score
                   495
E value
                   3.0e-50
                   95
Match length
                   98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - upland cotton >gi_450505_emb CAA38026 (X54091)
                   ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                   223974
Seq. ID
                   LIB3165-060-Q1-K1-G12
Method
                   BLASTX
NCBI GI
                   g1781348
BLAST score
                   572
E value
                   3.0e-59
Match length
                   119
% identity
NCBI Description
                  (Y10380) homologous to plastidic aldolases [Solanum
```

tuberosum]



Seq. ID LIB3165-060-Q1-K1-G2 Method BLASTX NCBI GI q1170567 BLAST score 280 E value 3.0e-25 Match length 56 89 % identity NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi\_1085960\_pir\_\_S52648 INO1 protein - Citrus paradisi >gi\_602565\_emb\_CAA83565\_ (Z32632) INO1 [Citrus x paradisi] Seq. No. Seq. ID LIB3165-060-Q1-K1-G4 Method BLASTX NCBI GI a3687652 BLAST score 503 E value 3.0e-51 Match length 106 % identity NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata] 223977 Seq. No. Seq. ID LIB3165-060-Q1-K1-G5 Method BLASTX NCBI GI q1871192 BLAST score 140 E value 1.0e-08 Match length 64 % identity NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana] Seq. No. 223978 Seq. ID LIB3165-060-Q1-K1-G7 Method BLASTX NCBI GI g1352821 BLAST score 302 E value 8.0e-28 Match length 63 % identity 94 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi\_450505\_emb\_CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum] Seq. No. 223979 Seq. ID LIB3165-060-Q1-K1-H1 Method BLASTX NCBI GI q2980770 BLAST score 260 E value 5.0e-23 Match length 67 % identity 78 NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

31797



Seq. ID LIB3165-060-Q1-K1-H11 Method BLASTX NCBI GI q131393 BLAST score 350 E value 3.0e-33 Match length 106 % identity 72 NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi\_100360\_pir\_\_S15005 photosystem II oxygen-evolving complex protein 2 - common tobacco >gi\_19911\_emb\_CAA39039.1\_ (X55354) photosystem II 23kDa polypeptide [Nicotiana tabacum] Seq. No. 223981 Seq. ID LIB3165-060-Q1-K1-H12 Method BLASTX NCBI GI q267122 BLAST score 422 E value 1.0e-41 Match length 100 77 % identity NCBI Description THIOREDOXIN H-TYPE (TRX-H) >gi 478400 pir JQ2242 thioredoxin h - Arabidopsis thaliana >gi\_16552\_emb\_CAA78462\_ (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi\_1388080 (U35827) thioredoxin h [Arabidopsis thalianal Seq. No. 223982 Seq. ID LIB3165-060-Q1-K1-H4 Method BLASTX NCBI GI g120659 BLAST score 396 E value 1.0e-38 Match length 79 % identity 94 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST >gi\_81721\_pir\_\_B24796 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13), chloroplast - white mustard (fragment) >gi\_829288\_emb\_CAA27845\_ (X04302) chloroplast GAPDH (233aa) [Sinapis alba] 223983 Seq. No. Seq. ID LIB3165-060-Q1-K1-H6 Method BLASTX NCBI GI g1749546 BLAST score 222 E value 3.0e-18 Match length 77 % identity 60 NCBI Description (D89169) similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces

pombe]

Seq. No.

Seq. ID LIB3165-060-Q1-K1-H7



```
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  320
E value
                  8.0e-30
Match length
                  63
                  97
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  223985
Seq. ID
                  LIB3165-060-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4406530
BLAST score
                  259
E value
                  5.0e-26
Match length
                  92
% identity
                  74
NCBI Description (AF126870) rubisco activase [Vigna radiata]
Seq. No.
                  223986
Seq. ID
                  LIB3166-001-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4102600
BLAST score
                  543
E value
                  9.0e-56
Match length
                  124
% identity
                  86
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                  223987
Seq. ID
                  LIB3166-001-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2584721
BLAST score
                  631
E value
                  4.0e-66
Match length
                  139
% identity
                  83
NCBI Description (Y10157) sulfite reductase [Arabidopsis thaliana]
Seq. No.
                  223988
Seq. ID
                  LIB3166-001-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  g967125
BLAST score
                  691
E value
                  4.0e-73
Match length
                  135
% identity
                  96
NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]
```

Seq. ID LIB3166-001-Q1-K1-A3

Method BLASTX
NCBI GI g1263291
BLAST score 556



```
E value
                     2.0e-57
Match length
                     120
   % identity
                     87
  NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
                     223990
  Seq. No.
  Seq. ID
                     LIB3166-001-Q1-K1-A5
  Method
                     BLASTX
  NCBI GI
                     q3169182
  BLAST score
                     360
  E value
                     2.0e-34
  Match length
                     78
  % identity
                     85
  NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     223991
  Seq. ID
                     LIB3166-001-Q1-K1-A6
  Method
                     BLASTX
  NCBI GI
                     q4455202
  BLAST score
                     392
  E value
                     5.0e-38
  Match length
                     106
  % identity
                     73
  NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]
  Seq. No.
                     223992
  Seq. ID
                     LIB3166-001-Q1-K1-A8
  Method
                     BLASTX
  NCBI GI
                     g2191129
  BLAST score
                     301
  E value
                     2.0e-27
  Match length
                     135
  % identity
  NCBI Description
                    (AF007269) similar to SPF1 DNA-binding protein [Arabidopsis
                     thaliana]
  Seq. No.
                     223993
  Seq. ID
                     LIB3166-001-Q1-K1-A9
  Method
                     BLASTX
  NCBI GI
                     g3046815
  BLAST score
                     544
  E value
                     7.0e-56
  Match length
                     130
  % identity
                     82
  NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
  Seq. No.
                     223994
  Seq. ID
                     LIB3166-001-Q1-K1-B1
  Method
                     BLASTX
  NCBI GI
                     g3122116
  BLAST score
                     296
```

E value 8.0e-27 Match length 132 % identity 48

NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG

>gi 2660540 emb CAA05102 (AJ001932) cell cycle protein

[Helicobacter felis]



```
223995
Seq. No.
                  LIB3166-001-Q1-K1-B10
Seq. ID
                  BLASTX
Method
                  g3023195
NCBI GI
                  605
BLAST score
                  5.0e-63
E value
                  135
Match length
                  88
% identity
                  14-3-3-LIKE PROTEIN B (SGF14B) >gi 1575727 (U70534) SGF14B
NCBI Description
                  [Glycine max]
                  223996
Seq. No.
                  LIB3166-001-Q1-K1-B11
Seq. ID
                  BLASTX
Method
                  g2541876
NCBI GI
                  221
BLAST score
                  5.0e-18
E value
                  76
Match length
                   51
% identity
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
                   223997
Seq. No.
                  LIB3166-001-Q1-K1-B3
Seq. ID
                  BLASTX
Method
                   g3608485
NCBI GI
BLAST score
                   649
                   3.0e-68
E value
Match length
                   127
                   94
% identity
NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]
                   223998
Seq. No.
                   LIB3166-001-Q1-K1-B7
Seq. ID
                   BLASTX
Method
                   g886116
NCBI GI
BLAST score
                   516
                   1.0e-52
E value
                   131
Match length
% identity
                   (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
NCBI Description
                   (AF051338) xyloglucan endotransglycosylase related protein
                   [Arabidopsis thaliana]
                   223999
Seq. No.
                   LIB3166-001-Q1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3955021
                   174
BLAST score
                   2.0e-12
E value
                   35
Match length
% identity
                   89
                   (AJ010811) HB2 homeodomain protein [Populus tremula x
```

NCBI Description

Populus tremuloides]



```
LIB3166-001-Q1-K1-C1
Seq. ID
Method
                  BLASTX
                  q3790567
NCBI GI
BLAST score
                  196
E value
                  4.0e-15
                  116
Match length
                  36
% identity
                  (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
NCBI Description
                  thaliana]
                  224001
Seq. No.
                  LIB3166-001-Q1-K1-C11
Seq. ID
Method
                  BLASTX
                  g1495804
NCBI GI
BLAST score
                  631
E value
                  4.0e-66
Match length
                  137
                  86
% identity
                  (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
Seq. No.
                  224002
                  LIB3166-001-Q1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1170504
BLAST score
                  175
                  1.0e-12
E value
Match length
                   68
                   49
% identity
                  EUKARYOTIC INITIATION FACTOR (ISO) 4F SUBUNIT P82
NCBI Description
                   (IEIF-(ISO)4F P82) >gi 452440 (M95747) initiation factor
                   (iso) 4f p82 subunit [Triticum aestivum]
                   224003
Seq. No.
                  LIB3166-001-Q1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455340
BLAST score
                   235
E value
                   1.0e-19
Match length
                   65
% identity
NCBI Description (AL035522) putative protein [Arabidopsis thaliana]
Seq. No.
                   224004
                   LIB3166-001-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1408471
BLAST score
                   511
                   5.0e-52
E value
                   113
Match length
                   81
% identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
```

Seq. ID LIB3166-001-Q1-K1-C6

Method BLASTX



```
q3021355
NCBI GI
BLAST score
                  409
                   5.0e-40
E value
                  89
Match length
% identity
                  88
                   (AJ005081) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                  tetragonoloba]
                  224006
Seq. No.
                  LIB3166-001-Q1-K1-C7
Seq. ID
Method
                  BLASTX
                   g2829918
NCBI GI
BLAST score
                   548
                   2.0e-56
E value
                  129
Match length
                   81
% identity
                  (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
                   224007
Seq. No.
                  LIB3166-001-Q1-K1-C8
Seq. ID
Method
                   BLASTX
                   g4314378
NCBI GI
                   343
BLAST score
                   3.0e-32
E value
Match length
                   136
% identity
                   51
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                   224008
Seq. No.
                   LIB3166-001-Q1-K1-D10
Seq. ID
Method
                   BLASTX
                   q4263712
NCBI GI
                   408
BLAST score
                   6.0e-40
E value
Match length
                   98
% identity
                   77
                   (ACO06223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   224009
Seq. No.
                   LIB3166-001-Q1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1706482
BLAST score
                   169
                   6.0e-12
E value
Match length
                   107
% identity
                   40
                   DNA LIGASE IV (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))
NCBI Description
                   >qi 860937 emb CAA58467 (X83441) DNA ligase IV [Homo
                   sapiens] >gi_4504997_ref_NP_002303.1_pLIG4_ ligase IV, DNA,
                   ATP-dependent
                   224010
Seq. No.
                   LIB3166-001-Q1-K1-D3
Seq. ID
```

31803

BLASTX

g2459429

Method

NCBI GI



```
502
BLAST score
E value
                   6.0e-51
                  126
Match length
                  71
% identity
                  (AC002332) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224011
Seq. No.
                  LIB3166-001-Q1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2501572
                  387
BLAST score
                   2.0e-37
E value
                  107
Match length
                   63
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi 1350545
NCBI Description
                   (L47118) EMB8 gene product [Picea glauca]
                   224012
Seq. No.
                  LIB3166-001-Q1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g310587
                   160
BLAST score
                   5.0e-11
E value
                   51
Match length
% identity
                   65
                  (L20864) ascorbate peroxidase [Spinacia oleracea]
NCBI Description
                   >gi 1384110_dbj_BAA12890_ (D85864) cytosolic ascorbate
                   peroxidase [Spinacia oleracea]
                   224013
Seq. No.
                   LIB3166-001-Q1-K1-D7
Seq. ID
Method
                   BLASTX
                   q4539348
NCBI GI
BLAST score
                   142
                   9.0e-09
E value
Match length
                   50
% identity
                   80-
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224014
                   LIB3166-001-Q1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4249410
BLAST score
                   563
E value
                   4.0e-58
Match length
                   128
% identity
                  (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
                   224015
Seq. No.
                   LIB3166-001-Q1-K1-E11
Seq. ID
Method
                   BLASTX
                   g2344901
NCBI GI
                   252
BLAST score
                   8.0e-22
E value
```

84

64

Match length % identity



```
(AC002388) serine/threonine protein kinase isolog
NCBI Description
                  [Arabidopsis thaliana]
                  224016
Seq. No.
                  LIB3166-001-Q1-K1-E12
Seq. ID
                  BLASTX
Method
                  g3775989
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
                  137
Match length
                  75
% identity
                  (AJ010458) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  224017
Seq. No.
                  LIB3166-001-Q1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4206789
                  457
BLAST score
                  9.0e-46
E value
Match length
                  129
                  71
% identity
                  (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis
NCBI Description
                  thaliana]
                  224018
Seq. No.
                  LIB3166-001-Q1-K1-E7
Seq. ID
                  BLASTX
Method
                  g4204313
NCBI GI
                  481
BLAST score
                  2.0e-48
E value
                  107
Match length
                   83
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   224019
Seq. No.
Seq. ID
                  LIB3166-001-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   q136636
BLAST score
                   469
                   4.0e-47
E value
Match length
                   87
                   98
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                   >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                   Arabidopsis thaliana >gi_442594 pdb 1AAK Ubiquitin
                   Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894 pdb 2AAK
                   Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                   >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                   thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme
                   [Arabidopsis thaliana]
```

LIB3166-001-Q1-K1-F10 Seq. ID

Method BLASTX NCBI GI q479406



```
404
BLAST score
                  5.0e-50
E value
                  119
Match length
                  62
% identity
                  chlorophyll a/b-binding protein - garden pea
NCBI Description
                  >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
                  224021
Seq. No.
                  LIB3166-001-Q1-K1-F11
Seq. ID
Method
                  BLASTX
                  g3281846
NCBI GI
                  176
BLAST score
                  1.0e-12
E value
                  132
Match length
                  33
% identity
                  (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
NCBI Description
                  224022
Seq. No.
                  LIB3166-001-Q1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3281848
                  188
BLAST score
                  4.0e-14
E value
                  132
Match length
                  46
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  224023
Seq. No.
                  LIB3166-001-Q1-K1-F5
Seq. ID
                  BLASTX
Method
                  g2218152
NCBI GI
BLAST score
                   693
                   2.0e-73
E value
Match length
                  136
                   90
% identity
NCBI Description
                   (AF005279) type IIIa membrane protein cp-wap13 [Vigna
                  unguiculata]
                   224024
Seq. No.
Seq. ID
                  LIB3166-001-Q1-K1-G12
Method
                  BLASTX
NCBI GI
                   q3218467
                   221
BLAST score
                   5.0e-18
E value
Match length
                   138
% identity
NCBI Description (AJ006529) putative phosphatase [Gallus gallus]
                   224025
Seq. No.
                   LIB3166-001-Q1-K1-G2
Seq. ID
Method
                   BLASTX
```

NCBI GI g1854386
BLAST score 487
E value 3.0e-49
Match length 137
% identity 68



```
(AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                    viniferal
Seq. No.
                    224026
Seq. ID
                    LIB3166-001-Q1-K1-G3
Method
                    BLASTX
NCBI GI
                    q2780194
                    546
BLAST score
E value
                    4.0e-56
Match length
                    123
                    58
% identity
                   (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
                    224027
Seq. No.
                    LIB3166-001-Q1-K1-G5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4262250
BLAST score
                    370
                    2.0e-35
E value
                    108
Match length
                    74
% identity
                   (AC006200) putative aldolase [Arabidopsis thaliana]
NCBI Description
                    224028
Seq. No.
                    LIB3166-001-Q1-K1-G6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3859116
                    360
BLAST score
E value
                    2.0e-34
                    120
Match length
                    59
% identity
NCBI Description (AF031609) unknown [Oryza sativa]
                    224029
Seq. No.
                    LIB3166-001-Q1-K1-G8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1946369
BLAST score
                    142
                     9.0e-09
E value
Match length
                    84
% identity
                     44
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
                    224030
Seq. No.
                    LIB3166-001-Q1-K1-G9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1346769
BLAST score
                    501
E value
                    8.0e-51
Match length
                    136
                     65
% identity
NCBI Description
                    PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
                    >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase
[Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase
[Homo sapiens] >gi_4506043_ref_NP_002717.1_pPREP_ prolyl
```

endopeptidase



```
Seq. No.
                  224031
                  LIB3166-001-Q1-K1-H2
Seq. ID
Method
                  BLASTX
                  g3402704
NCBI GI
BLAST score
                  344
E value
                  2.0e-32
Match length
                  119
% identity
                   66
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  224032
Seq. No.
Seq. ID
                  LIB3166-001-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g421836
BLAST score
                  603
E value
                  8.0e-63
Match length
                  139
                  84
% identity
                  G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040
NCBI Description
                   (M96855) GF14 [Arabidopsis thaliana]
                  2240,33
Seq. No.
                  LIB3166-001-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2252631
                   1.28
BLAST score
E value
                   1.0e-10
                   63
Match length
                   49
% identity
                  (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224034
                  LIB3166-001-Q1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3319342
BLAST score
                   164
E value
                   2.0e-11
Match length
                   45
                   64
% identity
                  (AF077407) similar to mitochondrial carrier proteins (Pfam:
NCBI Description
                   mit carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                   thaliana]
                   224035
Seq. No.
Seq. ID
                   LIB3166-001-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1352076
BLAST score
                   162
E value
                   4.0e-11
Match length
                   134
% identity
                   33
                  BETA-GALACTOSIDASE (LACTASE) >gi 144746 (M35107)
NCBI Description
                   beta-D-galactosidase (cbgA) [Clostridium acetobutylicum]
```

Seq. ID LIB3166-001-Q1-K1-H8

Method BLASTX



```
q4262225
NCBI GI
BLAST score
                  464
                  2.0e-46
E value
Match length
                  139
% identity
                  58
                  (AC006200) putative phosphatidic acid phosphatase
NCBI Description
                  [Arabidopsis thaliana]
                  224037
Seq. No.
                  LIB3166-001-Q1-K2-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4102600
BLAST score
                  543
E value
                  8.0e-56
                  124
Match length
                  86
% identity
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
                  224038
Seq. No.
                  LIB3166-001-Q1-K3-A1
Seq. ID
Method
                  BLASTX
                  g4102600
NCBI GI
                  543
BLAST score
                  8.0e-56
E value
Match length
                  124
% identity
                  86
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
                  224039
Seq. No.
                  LIB3166-001-Q1-K3-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1220196
BLAST score
                  535
                   7.0e-55
E value
Match length
                  115
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                   224040
                   LIB3166-001-Q1-K3-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122116
                   266
BLAST score
E value
                   2.0e-23
Match length
                   123
                   48
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG
NCBI Description
                   >gi_2660540_emb_CAA05102 (AJ001932) cell cycle protein
                   [Helicobacter felis]
                   224041
Seq. No.
                   LIB3166-001-Q1-K3-A7
Seq. ID
```

Method BLASTX
NCBI GI g3169182
BLAST score 360
E value 2.0e-34
Match length 78

NCBI Description

vinifera]



```
% identity
                  (AC004401) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224042
Seq. No.
                  LIB3166-001-Q1-K3-B1
Seq. ID
                  BLASTX
Method
                  q3608485
NCBI GI
                  597
BLAST score
                  4.0e-62
E value
                  117
Match length
                  95
% identity
                  (AF088915) proteasome beta subunit [Petunia x hybrida]
NCBI Description
Seq. No.
                  224043
Seq. ID
                  LIB3166-001-Q1-K3-B11
Method
                  BLASTX
                  q3859116
NCBI GI
BLAST score
                  223
                  6.0e-29
E value
Match length
                  121
% identity
                  64
NCBI Description
                  (AF031609) unknown [Oryza sativa]
                  224044
Seq. No.
                  LIB3166-001-Q1-K3-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3790567
BLAST score
                  161
E value
                  5.0e-11
Match length
                  108
                  33
% identity
                  (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
NCBI Description
                  thaliana]
                  224045
Seq. No.
                  LIB3166-001-Q1-K3-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1408471
                  455
BLAST score
                  1.0e-45
E value
                  102
Match length
                  79
% identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
                   224046
Seq. No:
Seq. ID
                  LIB3166-001-Q1-K3-B5
Method
                  BLASTX
NCBI GI
                   q1854386
BLAST score
                   462
E value
                   2.0e-46
Match length
                  127
% identity
                   69
                   (AB001375) similar to soluble NSF attachment protein [Vitis
```

Seq. ID Method

224052

BLASTX

LIB3166-001-Q1-K3-C3



```
224047
Seq. No.
Seq. ID
                  LIB3166-001-Q1-K3-B7
Method
                  BLASTX
NCBI GI
                   q886116
BLAST score
                   481
                   1.0e-48
E value
Match length
                   124
                   69
% identity
                   (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
NCBI Description
                   (AF051338) xyloglucan endotransglycosylase related protein
                   [Arabidopsis thaliana]
Seq. No.
                   224048
                  LIB3166-001-Q1-K3-B9
Seq. ID
Method
                   BLASTX
                   g2829918
NCBI GI
BLAST score
                   511
E value
                   4.0e-52
                   121
Match length
                   80
% identity
                  (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
                   224049
Seq. No.
                   LIB3166-001-Q1-K3-C1
Seq. ID
Method
                   BLASTX
                   g1545805
NCBI GI
                   159
BLAST score
                   5.0e-11
E value
                   89
Match length
                   48
% identity
NCBI Description
                  (D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
                   224050
Seq. No.
                   LIB3166-001-Q1-K3-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4262225
BLAST score
                   304
                   6.0e-28
E value
Match length
                   108
% identity
                   51
NCBI Description
                   (AC006200) putative phosphatidic acid phosphatase
                   [Arabidopsis thaliana]
                   224051
Seq. No.
                   LIB3166-001-Q1-K3-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2459429
BLAST score
                   461
E value
                   3.0e-46
Match length
                   116
% identity
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
```



```
g4249410
NCBI GI
BLAST score
                  519
                  5.0e-53
E value
Match length
                  119
                  81
% identity
                  (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224053
Seq. No.
                  LIB3166-001-Q1-K3-C4
Seq. ID
                  BLASTX
Method
                  g3402704
NCBI GI
BLAST score
                  312
                  1.0e-28
E value
                  107
Match length
% identity
                  67
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224054
                  LIB3166-001-Q1-K3-C7
Seq. ID
                  BLASTX
Method
                  g2501572
NCBI GI
                  387
BLAST score
E value
                  2.0e-37
                  107
Match length
% identity
                  63
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
NCBI Description
                  (L47118) EMB8 gene product [Picea glauca]
                  224055
Seq. No.
                  LIB3166-001-Q1-K3-D1
Seq. ID
                  BLASTX
Method
                  g4206789
NCBI GI
                  517
BLAST score
                  7.0e-53
E value
                  123
Match length
                   82
% identity
                  (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis
NCBI Description
                  thaliana]
                   224056
Seq. No.
                  LIB3166-001-Q1-K3-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3281848
                  164
BLAST score
E value
                   2.0e-11
                  113
Match length
                   46
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                   224057
Seq. ID
                   LIB3166-001-Q1-K3-D7
Method
                  BLASTX
NCBI GI
                   q4204313
                   414
BLAST score
```

31812

9.0e-41

91

85

E value Match length

% identity

NCBI Description



```
(AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  224058
                  LIB3166-001-Q1-K3-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2218152
BLAST score
                  531
E value
                   2.0e-54
Match length
                  125
% identity
                   78
                  (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                  unquiculata]
Seq. No.
                   224059
Seq. ID
                   LIB3166-001-Q1-K3-E2
Method
                  BLASTX
NCBI GI
                   g2780194
BLAST score
                   336
E value
                   1.0e-41
Match length
                   107
                   86
% identity
                  (AJ003197) adenine nucleotide translocator [Lupinus albus]
NCBI Description
                   224060
Seq. No.
Seq. ID
                   LIB3166-001-Q1-K3-E7
Method
                   BLASTX
NCBI GI
                   q4262250
BLAST score
                   312
                   9.0e-29
E value
                   96
Match length
                   72
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
                   224061
Seq. No.
Seq. ID
                   LIB3166-001-Q1-K3-F2
Method
                   BLASTX
NCBI GI
                   q1399273
BLAST score
                   619
E value
                   9.0e-65
Match length
                   123
                   94
% identity
                  (U31834) calmodulin-domain protein kinase CDPK isoform 5
NCBI Description
                   [Arabidopsis thaliana] >gi 3080419 emb_CAA18738_ (AL022604)
                   calmodulin-domain protein kinase CDPK isoform 5 (CPK5)
                   [Arabidopsis thaliana]
                   224062
Seq. No.
                   LIB3166-001-Q1-K3-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g98554
BLAST score
                   150
                   9.0e-10
E value
                   119
Match length
                   34
% identity
                   beta-galactosidase (EC 3.2.1.23) - Clostridium
```

31813

acetobutylicum

Method

NCBI GI

BLASTX

g310587



```
224063
Seq. No.
Seq. ID
                   LIB3166-001-Q1-K3-F8
Method
                   BLASTX
NCBI GI
                   q4455202
BLAST score
                   327
                   2.0e-30
E value
                   109
Match length
% identity
                   60
NCBI Description
                   (AL035440) putative APG protein [Arabidopsis thaliana]
                   224064
Seq. No.
                   LIB3166-001-Q1-K3-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2191129
BLAST score
                   225
                   1.0e-18
E value
Match length
                   115
% identity
                   51
NCBI Description
                   (AF007269) similar to SPF1 DNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   224065
Seq. ID
                   LIB3166-001-Q1-K3-G3
Method
                   BLASTX
                   g4455340
NCBI GI
BLAST score
                   172
E value
                   2.0e-12
Match length
                   64
% identity
                   58
                  (AL035522) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224066
                   LIB3166-001-Q1-K3-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3021355
BLAST score
                   409
                   4.0e-40
E value
Match length
                   89
                   88
% identity
                   (AJ005081) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                   tetragonoloba]
                   224067
Seq. No.
Seq. ID
                   LIB3166-001-Q1-K3-H7
Method
                   BLASTX
NCBI GI
                   q4314378
BLAST score
                   293
E value
                   2.0e-26
Match length
                   124
% identity
                   48
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224068
Seq. ID
                   LIB3166-001-Q1-K3-H8
```

NCBI GI

E value

BLAST score



```
143
 BLAST score
                    6.0e-09
 E value
 Match length
                    51
                    59
 % identity
                    (L20864) ascorbate peroxidase [Spinacia oleracea]
 NCBI Description
                    >gi 1384110_dbj_BAA12890_ (D85864) cytosolic ascorbate
                    peroxidase [Spinacia oleracea]
                    224069
 Seq. No.
                    LIB3166-002-Q1-K1-A10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4539301
 BLAST score
                    247
                    3.0e-21
 E value
                    68
 Match length
                    74
 % identity
                   (AL049480) putative mitochondrial protein [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    224070
                    LIB3166-002-Q1-K1-A2
 Seq. ID
 Method
                    BLASTX
                    g2827524
 NCBI GI
                    366
 BLAST score
 E value
                    3.0e-35
                    77
 Match length
 % identity
                    82
                   (AL021633) predicted protein [Arabidopsis thaliana]
 NCBI Description
                    224071
 Seq. No.
 Seq. ID
                    LIB3166-002-Q1-K1-A3
 Method
                    BLASTX
 NCBI GI
                    g3249081
 BLAST score
                    347
                    9.0e-33
 E value
 Match length
                    136
 % identity
                    11
                    (AC004473) Strong similarity to AROGP2 gene gb 1762634 from
MCBI Description
                    Lycopersicon esculentum. [Arabidopsis thaliana]
 Seq. No.
                    224072
                    LIB3166-002-Q1-K1-A4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4510430
 BLAST score
                    498
 E value
                    2.0e-50
 Match length
                    107
 % identity
                   (AC006929) unknown protein, 3' partial [Arabidopsis
 NCBI Description
                    thaliana]
                    224073
 Seq. No.
                    LIB3166-002-Q1-K1-A6
 Seq. ID
                    BLASTX
 Method
```

g2558938

9.0e-20

NCBI Description



```
Match length
                   55
% identity
                  (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
                  224074
Seq. No.
                  LIB3166-002-Q1-K1-A7
Seq. ID
Method
                  BLASTX
                  g4105782
NCBI GI
                  293
BLAST score
                  2.0e-26
E value
                   67
Match length
                  87
% identity
                  (AF049922) PGP169-12 [Petunia x hybrida]
NCBI Description
                  224075
Seq. No.
                  LIB3166-002-Q1-K1-A8
Seq. ID
Method
                  BLASTX
                  g3461846
NCBI GI
BLAST score
                   372
                  1.0e-35
E value
                  108
Match length
                   30
% identity
                  (AC005315) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   224076
Seq. No.
Seq. ID
                   LIB3166-002-Q1-K1-A9
                   BLASTX
Method
                   q1762428
NCBI GI
                   356
BLAST score
                   8.0e-34
E value
Match length
                   94
                   68
% identity
                  (U59467) aromatic rich glycoprotein JP630 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   224077
                   LIB3166-002-Q1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3688123
BLAST score
                   395
E value
                   2.0e-38
Match length
                   120
% identity
                  (AJ006293) granule-bound starch synthase [Antirrhinum
NCBI Description
                   majus]
Seq. No.
                   224078
                   LIB3166-002-Q1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g418507
BLAST score
                   167
E value
                   1.0e-11
                   71
Match length
% identity
                   48
                   S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE
```

METHYLTRANSFERASE >gi\_541097\_pir S40872 hypothetical



protein f161 - Escherichia coli >gi\_305032 (L19201)
ORF\_f161 [Escherichia coli] >gi\_1336002 (U56082)
S-adenosylmethionine:2-demethylmenaquinone
methyltransferase [Escherichia coli] >gi\_1790364 (AE000467)
menaquinone biosynthesis, unknown [Escherichia coli]

224079 Seq. No. LIB3166-002-Q1-K1-B2 Seq. ID Method BLASTX q3688123 NCBI GI BLAST score 352 2.0e-33 E value Match length 122 % identity 61

NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum

majus]

Seq. No. 224080

Seq. ID LIB3166-002-Q1-K1-B3

Method BLASTX
NCBI GI g3559811
BLAST score 498
E value 2.0e-50
Match length 137
% identity 72

NCBI Description (AJ010735) grl-protein [Arabidopsis thaliana]

Seq. No. 224081

Seq. ID LIB3166-002-Q1-K1-B4

Method BLASTX
NCBI GI g1483563
BLAST score 157
E value 1.0e-10
Match length 39
% identity 74

NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No. 224082

Seq. ID LIB3166-002-Q1-K1-B5

Method BLASTX
NCBI GI g1666096
BLAST score 453
E value 3.0e-45
Match length 129
% identity 73

NCBI Description (Y09113) dioxygenase [Marah macrocarpus]

Seq. No. 224083

Seq. ID LIB3166-002-Q1-K1-B8

Method BLASTX
NCBI GI g2827528
BLAST score 460
E value 5.0e-46
Match length 117
% identity 74

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]



83

NCBI Description (270677) thioredoxin [Ricinus communis]

% identity

```
224084
Seq. No.
                  LIB3166-002-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170031
                  634
BLAST score
                  2.0e-66
E value
                  135
Match length
                  89
% identity
NCBI Description
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
                   (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                  >gi_541940_pir__JQ2263 glutamate 1-semialdehyde
                  aminotransferase (EC 2.6.1.-) precursor - soybean
                  >gi 310567 (L12453) glutamate 1-semialdehyde
                  aminotransferase [Glycine max] >gi_747968 (U20260)
                  qlutamate 1-semialdehyde aminotransferase [Glycine max]
                  224085
Seq. No.
                  LIB3166-002-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1707018
BLAST score
                  456
                  1.0e-45
E value
Match length
                  132
                  70
% identity
NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]
                  224086
Seq. No.
                  LIB3166-002-01-K1-C10
Seq. ID
Method
                  BLASTX
                  g3859536
NCBI GI
BLAST score
                   626
                   2.0e-65
E value
Match length
                   125
% identity
NCBI Description (AF095453) asparagine synthetase [Arabidopsis thaliana]
Seq. No.
                   224087
                   LIB3166-002-Q1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4469020
BLAST score
                   469
E value
                   4.0e-47
Match length
                   123
% identity
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   224088
Seq. No.
                   LIB3166-002-Q1-K1-C12
Seq. ID
Method
                   BLASTX
                   q1255954
NCBI GI
                   534
BLAST score
E value
                   1.0e-54
                   118
Match length
```



```
Seq. No.
                   224089
Seq. ID
                   LIB3166-002-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   q3603401
BLAST score
                   288
E value
                   7.0e-26
Match length
                   126
                   49
% identity
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                   224090
                   LIB3166-002-Q1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2829870
BLAST score
                   275
                   2.0e-24
E value
Match length
                   117
                   58
% identity
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   224091
Seq. ID
                   LIB3166-002-Q1-K1-C4
Method
                   BLASTX
NCBI GI
                   q1708934
BLAST score
                   176
E value
                   9.0e-13
Match length
                   60
                   50
% identity
                   CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1 (RING FINGER
NCBI Description
                   PROTEIN MAT1) (MENAGE A TROIS) (CDK7/CYCLIN H ASSEMBLY
                   FACTOR) (P36) (P35) >gi_2137198_pir_ A57235 CDK-activating kinase p36 - mouse >gi_1015999 (U35249) CDK-activating
                   kinase assembly factor p36/MAT1 [Mus musculus]
Seq. No.
                   224092
Seq. ID
                   LIB3166-002-Q1-K1-C7
Method
                   BLASTX
NCBI GI
                   q1709007
BLAST score
                   187
E value
                    5.0e-14
                   107
Match length
% identity
                    40
                   O-SUCCINYLHOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE)
NCBI Description
                    >gi 607830 (U10904) O-succinylhomoserine sulfhydrylase
                    [Pseudomonas aeruginosa]
                   224093
Seq. No.
                   LIB3166-002-Q1-K1-D10
Seq. ID
                   {\tt BLASTX}
Method
NCBI GI
                   g3242789
BLAST score
                   549
```

2.0e-56E value 114 Match length 87 % identity

NCBI Description (AF055357) respiratory burst oxidase protein D [Arabidopsis

thaliana]



```
224094
Seq. No.
                  LIB3166-002-Q1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1469930
BLAST score
                  294
E value
                  1.0e-26
                  92
Match length
                  70
% identity
                  (U48777) fiber-specific acyl carrier protein [Gossypium
NCBI Description
                  hirsutum]
                  224095
Seq. No.
                  LIB3166-002-Q1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432859
BLAST score
                  326
                  2.0e-30
E value
                  106
Match length
% identity
                  61
                  (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224096
Seq. No.
                  LIB3166-002-Q1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024126
BLAST score
                  524
E value
                  1.0e-53
Match length
                  102
                  97
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 1655576 emb CAA95856 (Z71271) S-adenosyl-L-methionine
                  synthetase 1 [Catharanthus roseus]
Seq. No.
                  224097
Seq. ID
                  LIB3166-002-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  q3877579
BLAST score
                  216
E value
                  2.0e-17
Match length
                  108
% identity
                  49
NCBI Description
                  (Z82271) Similarity to Mouse kinensin-like protein KIF4
                   (SW:P33174); cDNA EST EMBL:D27320 comes from this gene;
                  cDNA EST EMBL: D27322 comes from this gene; cDNA EST
                  EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764
                  comes fr... >gi_3879321_emb_CAB07273_ (Z92811) Similarity
                  to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST
                  EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322
                  comes from this gene; cDNA EST EMBL: D27321 comes from this
                  gene; cDNA EST EMBL: D35764 comes fr
```

Seq. ID LIB3166-002-Q1-K1-D6

Method BLASTX NCBI GI g4455159 BLAST score 181



```
_1.0e-20
E value
Match length
                  72
                  62
% identity
                 (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                  224099
Seq. No.
                  LIB3166-002-Q1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4416347
BLAST score
                  416
E value
                  7.0e-41
Match length
                  87
                  92
% identity
                  (AF109403) MADS C-2 protein; MADS-box protein [Sinapis
NCBI Description
                  alba]
                  224100
Seq. No.
                  LIB3166-002-Q1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559358
                  208
BLAST score
                  2.0e-16
E value
Match length
                  65
                  57
% identity
                 (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224101
                  LIB3166-002-Q1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q516118
BLAST score
                  221
                  5.0e-18
E value
Match length
                  125
% identity
NCBI Description (L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]
                  224102
Seq. No.
                  LIB3166-002-Q1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  621
E value
                  6.0e-65
Match length
                  137
% identity
                  84
NCBI Description (AF027174) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
                  224103
Seq. No.
Seq. ID
                  LIB3166-002-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3046815
BLAST score
                  468
                   6.0e-47
E value
Match length
                  93
% identity
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
```

NCBI GI

BLAST score



```
224104
Seq. No.
Seq. ID
                   LIB3166-002-Q1-K1-E12
Method
                   BLASTX
                   g3953465
NCBI GI
                   116
BLAST score
                   8.0e-12
E value
                   91
Match length
                   51
% identity
                  (AC002328) F20N2.10 [Arabidopsis thaliana]
NCBI Description
                   224105
Seq. No.
                   LIB3166-002-Q1-K1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3434971
BLAST score
                   240
                   3.0e-20
E value
                   62
Match length
                   71
% identity
                  (AB008105) ethylene responsive element binding factor 3
NCBI Description
                   [Arabidopsis thaliana]
                   224106
Seq. No.
                   LIB3166-002-Q1-K1-E5
Seq. ID
Method
                   BLASTX
                   g2982303
NCBI GI
BLAST score
                   205
                   4.0e-16
E value
                   46
Match length
                   87
% identity
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
                   224107
Seq. No.
                   LIB3166-002-Q1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4432857
BLAST score
                   190
                   2.0e-14
E value
                   106
Match length
% identity
                   46
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   224108
Seq. No.
                   LIB3166-002-Q1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4049348
BLAST score
                   271
                   2.0e-26
E value
Match length
                   136
                   46
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                   224109
                   LIB3166-002-Q1-K1-E9
Seq. ID
                   {\tt BLASTX}
Method
```

g3983665 516



```
1.0e-52
E value
Match length
                   129
                   80
% identity
                  (AB011271) importin-beta2 [Oryza sativa]
NCBI Description
                   224110
Seq. No.
                   LIB3166-002-Q1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3834310
BLAST score
                   520
                   1.0e-53
E value
Match length
                   115
                   96
% identity
                   (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                   gb D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]
                   224111
Seq. No.
                   LIB3166-002-Q1-K1-F12
Seq. ID
Method
                   BLASTX
                   g3928084
NCBI GI
BLAST score
                   377
                   3.0e-36
E value
Match length
                   136
                   57
% identity
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   224112
Seq. No.
Seq. ID
                   LIB3166-002-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2970641
BLAST score
                   664
                   6.0e-70
E value
Match length
                   129
% identity
                   94
                   (AF052194) xyloglucan endotransglycosylase precursor
NCBI Description
                   [Actinidia deliciosa]
Seq. No.
                   224113
                   LIB3166-002-Q1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3434973
BLAST score
                   219
E value
                   8.0e-18
Match length
                   76
% identity
                   61
                   (AB008106) ethylene responsive element binding factor 4
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   224114
```

Šeq. ID LIB3166-002-Q1-K1-F5

BLASTX Method NCBI GI g1076515 BLAST score 258 E value 2.0e-22



```
115
Match length
                   49
% identity
                  pectinesterase precursor - kidney bean
NCBI Description
                  >gi_732913_emb_CAA59482_ (X85216) pectinesterase [Phaseolus
                  vulgaris]
Seq. No.
                   224115
                  LIB3166-002-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2642448
BLAST score
                   384
                   3.0e-37
E value
Match length
                   118
                   29
% identity
NCBI Description
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
                  >gi 3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
                   224116
Seq. No.
Seq. ID
                  LIB3166-002-Q1-K1-G10
Method
                  BLASTX
                   g710626
NCBI GI
BLAST score
                   287
                   9.0e-26
E value
Match length
                   86
                   65
% identity
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >qi 3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
                   224117
Seq. No.
                   LIB3166-002-Q1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g710626
BLAST score
                   187
E value
                   3.0e-14
                   79
Match length
                   53
% identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
Seq. No.
                   224118
Seq. ID
                   LIB3166-002-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   g4572679
BLAST score
                   388
E value
                   1.0e-37
Match length
                   106
% identity
                   69
```

NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition

motif [Arabidopsis thaliana]

Seq. No. 224119

Seq. ID LIB3166-002-Q1-K1-G4



```
Method
                  BLASTX
NCBI GI
                  q3962377
                  523
BLAST score
E value
                  2.0e-53
Match length
                  121
                  85
% identity
                 (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224120
Seq. ID
                  LIB3166-002-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  q4572679
BLAST score
                  234
                  8.0e-20
E value
Match length
                  67
% identity
                  66
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                  motif [Arabidopsis thaliana]
Seq. No.
                  224121
                  LIB3166-002-Q1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1332579
BLAST score
                  393
                  2.0e-56
E value
Match length
                  121
                  10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  224122
                  LIB3166-002-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266946
BLAST score
                  233
E value
                  9.0e-20
Match length
                  54
                  85
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO (LIGHT-INDUCED 34 KD
NCBI Description
                  PROTEIN) >gi_71143_pir__R5UBPO acidic ribosomal protein PO
                  - red goosefoot >gi_18141_emb_CAA33276 (X15206) 34kD
                  light-induced protein [Chenopodium rubrum]
                  224123
Seq. No.
Seq. ID
                  LIB3166-002-Q1-K1-H4
Method
                  BLASTX
NCBI GI
                  g100351
BLAST score
                  437
E value
                  2.0e-43
                  130
Match length
                  65
% identity
                  pathogenesis-related protein 4A - common tobacco
NCBI Description
                  >gi_19962_emb_CAA41437 (X58546) pathogenesis-related
                  protein 4A [Nicotiana tabacum]
```

Seq. ID LIB3166-002-Q1-K1-H6

Method BLASTX

E value

Match length

2.0e-37 78



```
q3955021
NCBI GI
                  423
BLAST score
E value
                  1.0e-41
                  96
Match length
                  85
% identity
                  (AJ010811) HB2 homeodomain protein [Populus tremula x
NCBI Description
                  Populus tremuloides]
                  224125
Seq. No.
                  LIB3166-002-Q1-K1-H7
Seq. ID
Method
                  BLASTX
                  g2738949
NCBI GI
BLAST score
                  335
                  1.0e-31
E value
                  68
Match length
% identity
                  90
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                  ananassa]
                  224126
Seq. No.
                  LIB3166-002-Q1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g70644
BLAST score
                  562
E value
                  5.0e-58
                  124
Match length
% identity
                  18
NCBI Description ubiquitin precursor - common sunflower (fragment)
Seq. No.
                  224127
Seq. ID
                  LIB3166-003-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q3757521
BLAST score
                  492
E value
                  9.0e-50
Match length
                  143
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                  224128
Seq. No.
Seq. ID
                  LIB3166-003-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g4539370
BLAST score
                  221
E value
                   3.0e-18
Match length
                  59
% identity
                   71
                  (AL049525) UDP-galactose 4-epimerase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   224129
Seq. No.
                  LIB3166-003-P1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g224293
BLAST score
                  386
```



```
% identity
NCBI Description histone H4 [Triticum aestivum]
                   224130
Seq. No.
                   LIB3166-003-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3335060
                   150
BLAST score
                   1.0e-09
E value
Match length
                   110
                   36
% identity
                   (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
NCBI Description
                   thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
                   224131
Seq. No.
                   LIB3166-003-P1-K1-B12
Seq. ID
                   BLASTX
Method
                   g2146797
NCBI GI
                   429
BLAST score
E value
                   2.0e-42
                   138
Match length
                   40
% identity
                   protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                   >gi_1134968 (U41385) protein disulphide isomerase PDI
                    [Ricinus communis] >gi_1587210_prf__2206331A protein
                   disulfide isomerase [Ricinus communis]
                   224132
Seq. No.
                   LIB3166-003-P1-K1-B2
Seq. ID
Method
                   BLASTX
                   q2244999
NCBI GI
                   220
BLAST score
                    7.0e-18
E value
                   96
Match length
                    47
% identity
                   (Z97341) similarity to phaseolin G-box binding protein PG2
NCBI Description
                    [Arabidopsis thaliana]
                    224133
Seq. No.
                    LIB3166-003-P1-K1-B8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g131399
```

Method BLASTX
NCBI GI g131399
BLAST score 442
E value 5.0e-44
Match length 105
% identity 79

NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE

TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi\_82277\_pir\_\_S00411

photosystem II 10K protein precursor - potato

>gi 21489\_emb\_CAA28450\_ (X04753) ST-LS1 protein [Solanum

tuberosum]

Seq. No. 224134

Seq. ID LIB3166-003-P1-K1-C1

Method BLASTX NCBI GI g3176726



```
BLAST score
                   299
                   4.0e-27
E value
Match length
                   82
% identity
                   76
                   (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                   224135
Seq. No.
Seq. ID
                   LIB3166-003-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q1174162
                   638
BLAST score
                   7.0e-67
E value
                   121
Match length
% identity
                   93
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                   thaliana] >gi 3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                   224136
Seq. No.
                   LIB3166-003-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4218011
BLAST score
                   518
E value
                   8.0e-53
Match length
                   130
% identity
                   75
                   (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi_4309721_gb_AAD15491_ (AC006439) putative
serine/threonine protein kinase [Arabidopsis thaliana]
                   224137
Seq. No.
                   LIB3166-003-P1-K1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3600031
BLAST score
                   226
E value
                   1.0e-18
Match length
                   111
% identity
                   (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
NCBI Description
                   acid aldolases [Arabidopsis thaliana]
Seq. No.
                   224138
                   LIB3166-003-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244734
BLAST score
                   710
                   2.0e-75
E value
Match length
                   142
                   99
% identity
                  (D88414) actin [Gossypium hirsutum]
NCBI Description
```

Seq. ID LIB3166-003-P1-K1-D10

Method BLASTX
NCBI GI g3122049
BLAST score 206



E value 1.0e-17 Match length 123 46 % identity DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) NCBI Description >gi\_1330236\_dbj\_BAA11189\_ (D78011) dihydropyrimidinase [Homo sapiens] >gi\_3608122 dbj\_BAA33067 (AB004678) dihydropyrimidinase [Homo sapiens] >gi 4503375 ref NP 001376.1\_pDPYS\_ dihydropyrimidinase 224140 Seq. No. Seq. ID LIB3166-003-P1-K1-D11 Method BLASTX q4455208 NCBI GI 554 BLAST score E value 5.0e-57 138 Match length % identity 78 NCBI Description (AL035440) putative protein [Arabidopsis thaliana] 224141 Seq. No. LIB3166-003-P1-K1-D4 Seq. ID Method BLASTX NCBI GI q466172 BLAST score 146 3.0e-09 E value Match length 61 52 % identity NCBI Description GTP-BINDING PROTEIN YPTM2 >gi 283056 pir B38202 ypt family - maize >gi 287835 emb CAA44919 (X63278) yptm2 [Zea mays] Seq. No. 224142 LIB3166-003-P1-K1-D8 Seq. ID Method BLASTX NCBI GI q3935168 BLAST score 223 E value 2.0e-25 Match length 122 54 % identity NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana] Seq. No. 224143 LIB3166-003-P1-K1-E6 Seq. ID Method BLASTX NCBI GI g3688191 BLAST score 201 E value 1.0e-15 Match length 84 % identity 52 (AJ010090) MAP3K alpha protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 224144

LIB3166-003-P1-K1-E7 Seq. ID

BLASTX Method NCBI GI g4115377 BLAST score 428 2.0e-42 E value



```
Match length
                  100
% identity
                   79
NCBI Description
                  (AC005967) unknown protein [Arabidopsis thaliana]
                  224145
Seq. No.
                  LIB3166-003-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115833
BLAST score
                  308
                   6.0e-44
E value
Match length
                  130
% identity
                   66
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                  224146
Seq. No.
                  LIB3166-003-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3142290
BLAST score
                  487
E value
                   3.0e-49
Match length
                  126
% identity
                  80
NCBI Description
                  (AC002411) Contains similarity to gb Z69902 from C.
                  elegans. [Arabidopsis thaliana]
                   224147
Seq. No.
Seq. ID
                  LIB3166-003-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2244865
BLAST score
                  158
E value
                  1.0e-10
Match length
                  127
% identity
                   33
                 (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   224148
Seq. No.
Seq. ID
                  LIB3166-003-P1-K1-G10
Method
                  BLASTX
NCBI GI
                   g3860263
BLAST score
                   330
                   9.0e - 31
E value
Match length
                  126
% identity
                   56
                  (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                  thaliana]
                   224149
Seq. No.
                  LIB3166-003-P1-K1-G2
Seq. ID
                  BLASTX
Method
```

NCBI GI g3201541
BLAST score 245
E value 2.0e-21
Match length 50
% identity 90

Seq. No.

Seq. ID

224155

LIB3166-003-P1-K1-H2



```
(AJ005077) TCTR2 protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  224150
                  LIB3166-003-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  243
E value
                   2.0e-34
Match length
                  100
                  79
% identity
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                  224151
Seq. No.
Seq. ID
                  LIB3166-003-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2245066
BLAST score
                  180
                   9.0e-14
E value
                   55
Match length
                   60
% identity
NCBI Description
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
                   224152
Seq. No.
                  LIB3166-003-P1-K1-G7
Seq. ID
Method
                  BLASTX .
                   g1730630
NCBI GI
BLAST score
                   207
                   2.0e-16
E value
                   134
Match length
                   37
% identity
                  HYPOTHETICAL 82.6 KD PROTEIN B0361.8 IN CHROMOSOME III
NCBI Description
                   >gi 458956 (U00031) similar to cytoplasmic domain of
                   synaptobrevin [Caenorhabditis elegans]
                   224153
Seq. No.
Seq. ID
                   LIB3166-003-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g1142621
BLAST score
                   219
                   9.0e-18
E value
Match length
                   139
% identity
                   44
                   (U18349) phaseolin G-box binding protein PG2 [Phaseolus
NCBI Description
                   vulgaris]
                   224154
Seq. No.
Seq. ID
                   LIB3166-003-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g1657948
BLAST score
                   180
E value
                   1.0e-13
Match length
                   37
% identity
                   86
                  (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
```



```
BLASTX
Method
NCBI GI
                  q1351135
BLAST score
                  280
                  2.0e-29
E value
                  90
Match length
                  75
% identity
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                  >gi_436792_emb_CAA50317_ (X70990) sucrose synthase
                  [Arabidopsis thaliana]
                  224156
Seq. No.
                  LIB3166-003-P1-K1-H6
Seq. ID
                  BLASTX
Method
                  g1657948
NCBI GI
                  137
BLAST score
                  9.0e-09
E value
                  41
Match length
                  66
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                  224157
Seq. No.
                  LIB3166-003-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g1174592
NCBI GI
BLAST score
                  734
                  4.0e-78
E value
Match length
                  142
                   99
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
Seq. No.
                   224158
                   LIB3166-004-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q586339
BLAST score
                   158
                   1.0e-10
E value
Match length
                   58
                   47
% identity
NCBI Description PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098
                   probable AMP-binding protein - yeast (Saccharomyces
                   cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c
                   [Saccharomyces cerevisiae]
                   224159
Seq. No.
                   LIB3166-004-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244916
BLAST score
                   160
E value
                   7.0e-11
Match length
                   131
                   31
% identity
NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]
```

224160

LIB3166-004-P1-K1-A6

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q2190548
BLAST score
                  229
E value
                  3.0e-21
Match length
                  81
                  65
% identity
                  (AC001229) EST gb ATTS1121 comes from this gene.
NCBI Description
                  [Arabidopsis thaliana]
                  224161
Seq. No.
                  LIB3166-004-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3551999
BLAST score
                  364
E value
                  7.0e-35 c
Match length
                  102
                  58
% identity
                  (AF085081) alcohol dehydrogenase A [Gossypium hirsutum]
NCBI Description
                  >gi_3552001 (AF085082) alcohol dehydrogenase A [Gossypium
                  hirsutum] >gi 4140628 (AF090163) alcohol dehydrogenase A
                  [Gossypium hirsutum] >gi_4140630 (AF090164) alcohol
                  dehydrogenase A [Gossypium hirsutum]
Seq. No.
                  224162
                  LIB3166-004-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914442
BLAST score
                  359
                  3.0e-34
E value
Match length
                  99
                  73
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >qi 1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  224163
                  LIB3166-004-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1351014
                  339
BLAST score
                  8.0e-32
E value
                  72
Match length
                  89
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207_ (D38010)
                  ribosomal protein S8 [Oryza sativa]
                  224164
Seq. No.
Seq. ID
                  LIB3166-004-P1-K1-B11
                  BLASTX
Method
NCBI GI
                  q3759184
BLAST score
                  272
                  5.0e-24
```

E value 121 Match length 50 % identity

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 224165



```
LIB3166-004-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1279542
BLAST score
                  505
E value
                  2.0e-51
Match length
                  118
                  89
% identity
NCBI Description
                  (Z71276) small GTPase [Mangifera indica]
                  224166
Seq. No.
                  LIB3166-004-P1-K1-B3
Seq. ID
Method
                  BLASTX
                  g4538939
NCBI GI
BLAST score
                  300
                  4.0e-52
E value
Match length
                  125
                  89
% identity
                  (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224167
                  LIB3166-004-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402683
BLAST score
                  146
                  3.0e-09
E value
Match length
                  39
                  74
% identity
NCBI Description
                  (AC004697) patatin-like protein [Arabidopsis thaliana]
Seq. No.
                  224168
                  LIB3166-004-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130024
BLAST score
                  350
E value
                   4.0e-33
Match length
                  103
% identity
                   62
                  DNA-binding protein ABF2 - wild oat
NCBI Description
                  >gi 1159879 emb CAA88331 (Z48431) DNA-binding protein
                   [Avena fatua]
Seq. No.
                  224169
Seq. ID
                  LIB3166-004-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2129604
BLAST score
                  210
E value
                   1.0e-16
Match length
                  58
% identity
                  74
NCBI Description
                  GTP-binding protein 1 - Arabidopsis thaliana
                  >gi_2129607_pir__S71584 GTP-binding protein ATBG1 -
                  Arabidopsis thaliana >gi_1184981 (U46924) ATGB1
                   [Arabidopsis thaliana]
```

Seq. ID LIB3166-004-P1-K1-C11

224170

Seq. No.



```
Method
                  BLASTX
NCBI GI
                  q3850583
BLAST score
                  330
E value
                  8.0e-31
Match length
                  125
% identity
                  56
                  (AC005278) Contains similarity to transcription initiation
NCBI Description
                  factor IIE, alpha subunit gb_X63468 from Homo sapiens.
                  [Arabidopsis thaliana]
Seq. No.
                  224171
                  LIB3166-004-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1931640
BLAST score
                  454
                  3.0e-45
E value
                  124
Match length
% identity
                  66
                  (U95973) Serine carboxypeptidase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  224172
Seq. No.
Seq. ID
                  LIB3166-004-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q2102696
BLAST score
                  228
                  8.0e-19
E value
Match length
                  110
                  40
% identity
NCBI Description
                  (U72761) karyopherin beta 3 [Homo sapiens]
                  >gi 4504909 ref NP 002262.1 pKPNB3 karyopherin (importin)
Seq. No.
                  224173
Seq. ID
                  LIB3166-004-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g3687243
BLAST score
                  249
E value
                  3.0e-21
Match length
                  68
% identity
                  72
                  (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
                  224174
Seq. No.
Seq. ID
                  LIB3166-004-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1173218
                  575
BLAST score
E value
                  2.0e-59
Match length
                  113
                  98
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
```

Seq. No. 224175

protein S15 [Arabidopsis thaliana] >gi\_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]



```
LIB3166-004-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  g232024
NCBI GI
                  301
BLAST score
                  2.0e-27
E value
                  85
Match length
                  69
% identity
                  PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland
NCBI Description
                  cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                  is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
                  224176
Seq. No.
                  LIB3166-004-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  q3068705
NCBI GI
                  201
BLAST score
                  7.0e-16
E value
                  64
Match length
                  69
% identity
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                  224177
Seq. No.
                  LIB3166-004-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  g1171579
NCBI GI
BLAST score
                  273
                  1.0e-24
E value
                   66
Match length
                   80
% identity
                  (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
                  224178
Seq. No.
                  LIB3166-004-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4185740
                   354
BLAST score
                   1.0e-33
E value
Match length
                  139
                   56
% identity
NCBI Description
                  (AF079999) putative glutamate receptor [Arabidopsis
                   thaliana]
                   224179
Seq. No.
                   LIB3166-004-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q541881
BLAST score
                   306
                   4.0e-28
E value
Match length
                   75
                   73
% identity
NCBI Description
                  MYB homolog transcription ATMYB2 - Arabidopsis thaliana
                   >gi 506189 dbj BAA03534 (D14712) ATMYB2 [Arabidopsis
```

thaliana]

thaliana] >gi\_2275197 (AC002337) Atmyb2 [Arabidopsis

NCBI GI

E value

BLAST score

g1531758

2.0e-12

174



```
224180
Seq. No.
                  LIB3166-004-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510375
                  460
BLAST score
                  5.0e-46
E value
                  116
Match length
                  77
% identity
NCBI Description
                  (AC007017) putative homeotic protein BEL1 [Arabidopsis
                  thaliana]
                  224181
Seq. No.
                  LIB3166-004-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2443891
BLAST score
                  163
                   3.0e-11
E value
Match length
                  116
                   49
% identity
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   224182
Seq. No.
                  LIB3166-004-P1-K1-G10
Seq. ID
                  BLASTX
Method
                   g2347199
NCBI GI
BLAST score
                   176
                   9.0e - 13
E value
                   72
Match length
                   64
% identity
                 (AC002338) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
                   224183
Seq. No.
                   LIB3166-004-P1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4538911
BLAST score
                   379
E value
                   1.0e-36
Match length
                   120
% identity
NCBI Description (ALO49482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   224184
                   LIB3166-004-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2970051
BLAST score
                   225
E value
                   1.0e-18
                   63
Match length
                   63
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                   224185
                   LIB3166-004-P1-K1-G4
Seq. ID
                   BLASTX
Method
```



Match length 36 78 % identity (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028) NCBI Description unknown protein [Arabidopsis thaliana] 224186 Seq. No. LIB3166-004-P1-K1-G6 Seq. ID BLASTX Method g1174592 NCBI GI 629 BLAST score 7.0e-66 E value Match length 118 97 % identity TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin NCBI Description - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum sativum] 224187 Seq. No. LIB3166-004-P1-K1-G7 Seq. ID BLASTX Method g3004555 NCBI GI BLAST score 316 4.0e-29 E value 136 Match length 5 % identity (AC003673) similar to salt inducible protein [Arabidopsis NCBI Description thaliana] 224188 Seq. No. LIB3166-004-P1-K1-H2 Seq. ID BLASTX Method g1653702 NCBI GI BLAST score 254 5.0e-22 E value 80 Match length 65 % identity NCBI Description (D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.] 224189 Seq. No. LIB3166-004-P1-K1-H5 Seq. ID Method BLASTX NCBI GI g3582342 BLAST score 278 E value 1.0e-24Match length 139 % identity (AC005496) putative flavonol 3-o-glucosyltransferase NCBI Description [Arabidopsis thaliana] 224190 Seq. No. LIB3166-005-P1-K1-A1 Seq. ID

BLASTX Method NCBI GI g3046696 BLAST score 289 E value 2.0e-37 113 Match length

NCBI Description



```
% identity
                  (AL022224) CTP synthase like protein [Arabidopsis thaliana]
NCBI Description
                  224191
Seq. No.
                  LIB3166-005-P1-K1-A11
Seq. ID
Method
                  BLASTX
                  q4056494
NCBI GI
                  438
BLAST score
E value
                   2.0e-43
Match length
                  108
                  76
% identity
                   (AC005896) putative protein translocase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   224192
                  LIB3166-005-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2262178
                   277
BLAST score
E value
                   1.0e-24
Match length
                   129
                   50
% identity
                  (AC002329) putative Mlo-like protein [Arabidopsis thaliana]
NCBI Description
                   224193
Seq. No.
                  LIB3166-005-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2642648
BLAST score
                   715
                   6.0e-76
E value
Match length
                   143
                   98
% identity
                   (AF033852) cytosolic heat shock 70 protein; HSC70-3
NCBI Description
                   [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat
                   shock 70 protein [Spinacia oleracea] >gi_2660770 (AF034617)
                   cytosolic heat shock 70 protein [Spinacia oleracea]
                   224194
Seq. No.
                   LIB3166-005-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2661021
BLAST score
                   594
E value
                   9.0e-62
Match length
                   117
% identity
                   95
NCBI Description (AF035255) catalase [Glycine max]
Seq. No.
                   224195
                   LIB3166-005-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1297190
BLAST score
                   413
E value
                   2.0e-40
Match length
                   103
                   77
% identity
```

(U53501) Theoretical protein with similarity to GenBank Accession Number L22302 serine/threonine protein kinase

Match length

% identity

123

76



## [Arabidopsis thaliana]

```
Seq. No.
                  224196
Seq. ID
                  LIB3166-005-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1345684
BLAST score
                  455
E value
                  2.0e-45
Match length
                  105
% identity
                  85
                  CATALASE ISOZYME 3 >gi 536787 emb CAA85426 (Z36977)
NCBI Description
                  catalase [Nicotiana plumbaginifolia]
Seq. No.
                  224197
                  LIB3166-005-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                  255
E value
                  6.0e-22
Match length
                  119
% identity
                  51
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  224198
Seq. ID
                  LIB3166-005-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3776559
BLAST score
                  323
E value
                  6.0e-30
Match length
                  109
% identity
                  54
                  (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  224199
Seq. ID
                  LIB3166-005-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g729092
BLAST score
                  662
E value
                  1.0e-69
Match length
                  134
                  92
% identity
NCBI Description
                  CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK)
                  >gi_477484_pir__A49082 calcium-dependent protein kinase
                  isoform AKI - Arabidopsis thaliana >gi 304105 (L14771)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                  224200
Seq. ID
                  LIB3166-005-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1168446
BLAST score
                  495
E value
                  4.0e-50
```

% identity

17



```
AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)
NCBI Description
                   >gi_1073840_pir__F64132 aminopeptidase N (pepN) homolog -
                   Haemophilus influenzae (strain Rd KW20) >gi_1574460
                   (U32835) aminopeptidase N (pepN) [Haemophilus influenzae
                   Rd]
                   224201
Seq. No.
                   LIB3166-005-P1-K1-B3
Seq. ID
Method
                   BLASTX
                   g1326161
NCBI GI
BLAST score
                   142
E value
                   1.0e-08
Match length
                   55
                   60
% identity
NCBI Description (U54703) dehydrin [Phaseolus vulgaris]
                   224202
Seq. No.
                   LIB3166-005-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g548770
BLAST score
                   165
                   1.0e-11
E value
Match length
                   63
                   60
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__ S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
NCBI Description
                   ribosomal protein L3 [Oryza sativa]
                   224203
Seq. No.
                   LIB3166-005-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q100200
BLAST score
                   160
E value
                   4.0e-11
Match length
                   72
% identity
                   51
NCBI Description chlorophyll a/b-binding protein type I precursor - tomato
Seq. No.
                   224204
                   LIB3166-005-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539348
BLAST score
                   359
                   4.0e-34
E value
                   123
Match length
% identity
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]
                   224205
Seq. No.
                   LIB3166-005-P1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g418854
BLAST score
                   622
E value
                   5.0e-65
                   131
Match length
```

31841

NCBI Description ubiquitin precursor - parsley >gi 288112 emb\_CAA45621\_



(X64344) polyubiquitin [Petroselinum crispum] >gi 288114\_emb\_CAA45622\_ (X64345) polyubiquitin [Petroselinum crispum]

224206 Seq. No. LIB3166-005-P1-K1-D1 Seq. ID Method BLASTX NCBI GI g225242 BLAST score 154 2.0e-10 E value Match length 36 % identity 86

NCBI Description ORF 1708 [Nicotiana tabacum]

224207

LIB3166-005-P1-K1-D11 Seq. ID Method BLASTX NCBI GI q1946220 BLAST score 180 E value 3.0e-13Match length 34 94 % identity

Seq. No.

(Z71979) kn1-like protein [Malus domestica] NCBI Description

Seq. No. 224208

LIB3166-005-P1-K1-D12 Seq. ID

Method BLASTX NCBI GI q3901012 BLAST score 199 E value 1.0e-15 Match length 44 75 % identity

(AJ130885) xyloglucan endotransglycosylase 1 [Fagus NCBI Description

sylvatica]

224209 Seq. No.

LIB3166-005-P1-K1-D5 Seq. ID

BLASTX Method NCBI GI g3249084 BLAST score 236 2.0e-34 E value 155 Match length 29 % identity

(AC004473) Similar to red-1 (related to thioredoxin) gene NCBI Description

qb X92750 from Mus musculus. ESTs gb AA712687 and gb\_Z37223 come from this gene [Arabidopsis thaliana]

224210 Seq. No.

Seq. ID LIB3166-005-P1-K1-D6

Method BLASTX NCBI GI g4559372 BLAST score 357 E value 6.0e - 34Match length 87 % identity

NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]

E value

Match length

4.0e-44

134



```
Seq. No.
                     224211
Seq. ID
                     LIB3166-005-P1-K1-E1
Method
                     BLASTX
NCBI GI
                     g1076708
BLAST score
                     619
E value
                     1.0e-64
Match length
                     126
% identity
                     28
NCBI Description
                     seed tetraubiquitin - common sunflower
                     >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
                     [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                     putative polyubiquitin [Arabidopsis thaliana]
                     >gi 1096513 prf 2111434A tetraubiquitin [Helianthus
                     annuus]
Seq. No.
                     224212
Seq. ID
                     LIB3166-005-P1-K1-E12
Method
                     BLASTX
NCBI GI
                     q3928095
BLAST score
                     399
E value
                     8.0e-54
Match length
                     138
                     76
% identity
NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                     224213
Seq. ID
                     LIB3166-005-P1-K1-E3
Method
                     BLASTX
NCBI GI
                     g951427
BLAST score
                     453
E value
                     3.0e-45
Match length
                     134
% identity
                     61
NCBI Description
                    (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
                     communis]
Seq. No.
                     224214
Seq. ID
                     LIB3166-005-P1-K1-E4
Method
                     BLASTX
NCBI GI
                     g951427
BLAST score
                     539
E value
                     3.0e-55
Match length
                     135
                     75
% identity
NCBI Description
                    (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
                     communis]
Seq. No.
                     224215
Seq. ID
                     LIB3166-005-P1-K1-E5
Method
                     BLASTX
NCBI GI
                     g134945
BLAST score
                     444
```



```
% identity
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                   (STEAROYL-ACP DESATURASE) (DELTA(9) STEAROYL-ACYL CARRIER
                   PROTEIN DESATURASE) >gi_66360_pir__OHCSAD
                   acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)
                   precursor - castor bean >gi_21093_emb_CAA39859_ (X56508)
acyl-[acyl-carrier protein] desatu [Ricinus communis]
                   >gi_228313_prf__1802405A stearoyl acyl carrier desaturase
                   [Ricinus communis]
Seq. No.
                   224216
Seq. ID
                   LIB3166-005-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q1703129
BLAST score
                   578
                   7.0e-60
E value
Match length
                   114
                   95
% identity
NCBI Description
                   ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis
                   thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis
                   thaliana]
Seq. No.
                   224217
Seq. ID
                   LIB3166-005-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q4455318
BLAST score
                   327
E value
                   9.0e-31
Match length
                   88
                   72
% identity
NCBI Description
                  (AL035528) glycine hydroxymethyltransferase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   224218
Seq. ID
                   LIB3166-005-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q3559816
BLAST score
                   699
E value
                   5.0e-74
Match length
                   142
% identity
                   93
NCBI Description (Y15782) transketolase 2 [Capsicum annuum]
Seq. No.
                   224219
Seq. ID
                   LIB3166-005-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g4105794
BLAST score
                   298
E value
                   5.0e-27
Match length
                   79
% identity
                   62
NCBI Description (AF049928) PGP224 [Petunia x hybrida]
```

Seq. No. 224220

Seq. ID LIB3166-005-P1-K1-F11

Method BLASTX NCBI GI g4468978



```
BLAST score
                  356
                  8.0e-34
E value
Match length
                  139
% identity
                  55
NCBI Description (AL035605) peroxidase-like protein [Arabidopsis thaliana]
Seq. No.
                  224221
Seq. ID
                  LIB3166-005-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q4063749
BLAST score
                  116
                  4.0e-11
E value
Match length
                  91
% identity
                  46
NCBI Description (AC005851) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  224222
Seq. ID
                  LIB3166-005-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g4455276
BLAST score
                  502
E value
                  6.0e-51
Match length
                  143
% identity
                  72
NCBI Description (AL035527) peptide transporter-like protein [Arabidopsis
                  thaliana]
                  224223
Seq. No.
                  LIB3166-005-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076715
BLAST score
                  196
E value
                  4.0e-15
Match length
                  86
% identity
                  41
NCBI Description abscisic acid-induced protein HVA22 - barley >gi 404589
                  (L19119) A22 [Hordeum vulgare]
Seq. No.
                  224224
Seq. ID
                  LIB3166-005-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1769903
BLAST score
                  347
                  9.0e-33
E value
Match length
                  140
% identity
                  54
NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]
                  224225
Seq. No.
Seq. ID
                  LIB3166-005-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  311
                  6.0e-56
E value
Match length
                  129
% identity
```

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]



```
224226
Seq. No.
                  LIB3166-005-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1694976
BLAST score
                   337
E value
                   1.0e-31
                  74
Match length
                   84
% identity
                   (Y09482) HMG1 [Arabidopsis thaliana]
NCBI Description
                   >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   224227
Seq. No.
                  LIB3166-005-P1-K1-H12
Seq. ID
                  BLASTX
Method
                   g3688123
NCBI GI
BLAST score
                   436
                   3.0e-43
E value
                   119
Match length
                   71
% identity
                  (AJ006293) granule-bound starch synthase [Antirrhinum
NCBI Description
                  majus]
                   224228
Seq. No.
                   LIB3166-005-P1-K1-H3
Seq. ID
Method
                   BLASTX
                   g3036951
NCBI GI
                   390
BLAST score
                   5.0e - 38
E value
                   74
Match length
                   100
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   224229
Seq. No.
Seq. ID
                   LIB3166-005-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q3193327
                   223
BLAST score
                   3.0e-18
E value
Match length
                   84
                   56
% identity
NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]
                   224230
Seq. No.
Seq. ID
                   LIB3166-005-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2494842
BLAST score
                   148
E value
                   3.0e-10
Match length
                   79
% identity
                   48
NCBI Description GLUCOSYLTRANSFERASE ALG6 >gi 2131171 pir S61985 ALG6
```

protein - yeast (Saccharomyces cerevisiae) >gi\_1150997 (U43491) hypothetical protein UNA544 [Saccharomyces

cerevisiae] >gi\_1420090\_emb\_CAA99190\_ (Z74910) ORF YOR002w

Seq. ID



## [Saccharomyces cerevisiae]

```
Seq. No.
                  224231
Seq. ID
                  LIB3166-005-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g170354
BLAST score
                  538
                  3.0e-55
E value
                  109
Match length
                  21
% identity
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                  224232
Seq. No.
                  LIB3166-005-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  g3928529
NCBI GI
                  152
BLAST score
                  9.0e-16
E value
                  88
Match length
% identity
                  53
                  (AB015502) alcohol dehydrogenase [Arabis hirsuta]
NCBI Description
                  224233
Seq. No.
                  LIB3166-005-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493146
BLAST score
                  223
                  3.0e-18
E value
                  61
Match length
                  75
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 755148
NCBI Description
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                   [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275)
                  vacuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.
                   224234
Seq. ID
                  LIB3166-005-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q2244732
BLAST score
                   751
                   4.0e-80
E value
Match length
                  141
                   99
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                   224235
Seq. No.
Seq. ID
                   LIB3166-006-P1-K1-A10
Method
                  BLASTX
NCBI GI
                   q2827709
BLAST score
                   280
E value
                   6.0e-25
Match length
                   133
% identity
                   47
NCBI Description (ALO21684) predicted protein [Arabidopsis thaliana]
Seq. No.
                   224236
```

LIB3166-006-P1-K1-A11



```
Method
                    BLASTX
NCBI GI
                    g3319921
BLAST score
                    190
                    1.0e-14
E value
Match length
                    60
                    63
% identity
NCBI Description
                   (AJ223388) Hev b 3 [Hevea brasiliensis]
                    >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3 [Hevea brasiliensis] >gi_3818475 (AF051317) small rubber
                    particle protein [Hevea brasiliensis]
                    224237
Seq. No.
                    LIB3166-006-P1-K1-A12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3335366
BLAST score
                    190
                    1.0e-14
E value
Match length
                    80
% identity
                    46
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
                    224238
Seq. No.
Seq. ID
                    LIB3166-006-P1-K1-A2
Method
                    BLASTX
NCBI GI
                    g3122785
BLAST score
                    410
                    2.0e-40
E value
Match length
                    88
% identity
                    92
NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi 2565340 (AF026079) ribosomal
                    protein S14 [Lupinus luteus]
                    224239
Seq. No.
Seq. ID
                    LIB3166-006-P1-K1-A3
                    BLASTX
Method
NCBI GI
                    q4249385
BLAST score
                    263
                    1.0e-44
E value
Match length
                    99
                    90
% identity
NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]
Seq. No.
                    224240
Seq. ID
                    LIB3166-006-P1-K1-A4
                    BLASTX
Method
NCBI GI
                    q117988
BLAST score
                    521
E value
                    3.0e-53
Match length
                    99
                    95
% identity
NCBI Description CYTOCHROME C >gi_65503 pir_CCCN cytochrome c - sea-island
                    cotton
```

Seq. No. 224241

Seq. ID LIB3166-006-P1-K1-A7

Method BLASTX



```
q4490321
NCBI GI
                    169
BLAST score
E value
                    4.0e-12
                    70
Match length
% identity
                    51
NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]
Seq. No.
                    224242
Seq. ID
                    LIB3166-006-P1-K1-A9
Method
                    BLASTX
NCBI GI
                    g2392769
BLAST score
                    145
E value
                    3.0e-12
Match length
                    87
% identity
                    52
                    (AC002534) putative histone deacetylase [Arabidopsis
NCBI Description
                    thaliana]
                    224243
Seq. No.
Seq. ID
                    LIB3166-006-P1-K1-B1
Method
                    BLASTX
NCBI GI
                    q4512698
BLAST score
                    548
E value
                    2.0e-56
Match length
                    112
% identity
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    224244
Seq. ID
                    LIB3166-006-P1-K1-B10
Method
                    BLASTX
NCBI GI
                    q1076365
BLAST score
                    218
E value
                    4.0e-18
Match length
                    76
% identity
                    57
NCBI Description pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis
                    thaliana >gi_2129666_pir__JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275_ (X81585) ATPME1 [Arabidopsis thaliana] >gi_903895 (U25649)
                    ATPME1 precursor [Arabidopsis thaliana]
                    224245
Seq. No.
                    LIB3166-006-P1-K1-B11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3790100
BLAST score
                    422
                    8.0e-42
E value
                    94
Match length
                    90
% identity
NCBI Description (AF095520) pyrophosphate-dependent phosphofructokinase beta
                    subunit [Citrus X paradisi]
                    224246
Seq. No.
```

Seq. ID LIB3166-006-P1-K1-B12

Method BLASTX NCBI GI g2244900



BLAST score 366 E value 2.0e-41 Match length 132 61 % identity (Z97338) similarity to hypothetical protein HYP1 -NCBI Description Arabidopsis [Arabidopsis thaliana] Seq. No. 224247 Seq. ID LIB3166-006-P1-K1-B2 Method BLASTX NCBI GI g125887 BLAST score 157 E value 1.0e-10 Match length 89

% identity 37
NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

>gi\_82092\_pir\_\_S04765 LAT52 protein precursor - tomato >gi\_295812\_emb\_CAA33854\_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 224248

Seq. ID LIB3166-006-P1-K1-B4

Method BLASTX
NCBI GI g1332579
BLAST score 486
E value 2.0e-52
Match length 115
% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 224249

Seq. ID LIB3166-006-P1-K1-B5

Method BLASTX
NCBI GI g4218122
BLAST score 276
E value 1.0e-24
Match length 95
% identity 61

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

Seq. No. 224250

Seq. ID LIB3166-006-P1-K1-C1

Method BLASTX
NCBI GI g2213643
BLAST score 250
E value 1.0e-28
Match length 91
% identity 71

NCBI Description (U57338) glossyl homolog [Oryza sativa]

Seq. No. 224251

Seq. ID LIB3166-006-P1-K1-C11

Method BLASTX
NCBI GI g2065531
BLAST score 254
E value 5.0e-22
Match length 81

E value

Match length

% identity

3.0e-12

124

39



```
% identity
NCBI Description
                   (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
Seq. No.
                    224252
Seq. ID
                    LIB3166-006-P1-K1-C12
Method
                    BLASTX
NCBI GI
                    q1345787
BLAST score
                    678
E value
                    1.0e-71
Match length
                    134
% identity
                    94
NCBI Description
                    CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)
                    >gi_567937_dbj_BAA05641_ (D26594) chalcone synthase
                    [Camellia sinensis]
Seq. No.
                    224253
Seq. ID
                    LIB3166-006-P1-K1-C4
Method
                    BLASTX
NCBI GI
                    q2244732
BLAST score
                    446
E value
                    2.0e-44
Match length
                    90
% identity
                    94
NCBI Description
                   (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.
                    224254
Seq. ID
                    LIB3166-006-P1-K1-C5
Method
                    BLASTX
NCBI GI
                    g2979551
BLAST score
                    174
E value
                    9.0e-13
Match length
                    57
% identity
                    65
NCBI Description
                    (AC003680) putative receptor protein kinase [Arabidopsis
                    thaliana]
~Seq. No.
                    224255
Seq. ID
                    LIB3166-006-P1-K1-C7
Method
                    BLASTX
NCBI GI
                    g128190
BLAST score
                    530
E value
                    2.0e-54
Match length
                    122
                    80
% identity
                   NITRATE REDUCTASE 2 (NR2) >gi_66205_pir__RDNTNS nitrate reductase (NADH) (EC 1.6.6.1) nia-2 - common tobacco
NCBI Description
                    >gi_19891_emb CAA32217 (X14059) nitrate reductase
                    [Nicotiana tabacum]
Seq. No.
                    224256
Seq. ID
                    LIB3166-006-P1-K1-D1
Method
                    BLASTX
NCBI GI
                    g4490341
BLAST score
                    172
```



```
(AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
                  224257
Seq. No.
Seq. ID
                  LIB3166-006-P1-K1-D10
Method
                  BLASTX
                  q3249084
NCBI GI
                  185
BLAST score
                  3.0e-14
E value
Match length
                  58
                  29
% identity
NCBI Description
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
                  gb X92750 from Mus musculus. ESTs gb_AA712687 and
                  gb Z37223 come from this gene [Arabidopsis thaliana]
                  224258
Seq. No.
                  LIB3166-006-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738285
                  278
BLAST score
E value
                  9.0e-25
Match length
                  69
                  75
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224259
Seq. No.
                  LIB3166-006-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g1173256
NCBI GI
BLAST score
                  629
                  7.0e-66
E value
Match length
                  123
% identity
                  98
                  40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   224260
Seq. No.
                  LIB3166-006-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                   173
                   7.0e-15
E value
Match length
                  54
                   81
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   224261
                  LIB3166-006-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1749596
BLAST score
                   252
E value
                   2.0e-27
Match length
                   101
% identity
                   61
                  (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT
NCBI Description
```

Accession Number P16638 [Schizosaccharomyces pombe]



```
Seq. No.
                  224262
Seq. ID
                  LIB3166-006-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2505870
BLAST score
                  575
E value
                  1.0e-59
Match length
                  128
% identity
                  89
NCBI Description
                 (Y12227) hypothetical protein [Arabidopsis thaliana]
                  224263
Seq. No.
                  LIB3166-006-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4468993
BLAST score
                  302
                  2.0e-27
E value
Match length
                  134
% identity
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
                  224264
Seq. No.
Seq. ID
                  LIB3166-006-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  125
                  6.0e-12
E value
Match length
                  59
                  67
% identity
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  224265
                  LIB3166-006-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1351974
BLAST score
                  568
E value
                  1.0e-58
Match length
                  110
                  100
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325
                  ADP-ribosylation factor - maize >gi 1076789 pir S53486
                  ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
                   (X80042) ADP-ribosylation factor [Zea mays]
Seq. No.
                  224266
                  LIB3166-006-P1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q125606
BLAST score
                  463
E value
                  2.0e-46
Match length
                  99
                  88
% identity
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463_pir__S12248
```

31853

>gi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum

pyruvate kinase (EC 2.7.1.40) - potato

tuberosum]

Method

NCBI GI

BLASTX

g1769903



```
224267
Seq. No.
Seq. ID
                  LIB3166-006-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g4102861
BLAST score
                  540
E value
                  2.0e-55
Match length
                  111
% identity
                  86
NCBI Description
                  (AF016893) copper/zinc-superoxide dismutase [Populus
                  tremuloides]
Seq. No.
                  224268
Seq. ID
                  LIB3166-006-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1895084
BLAST score
                  172
E value
                  3.0e-12
Match length
                  101
% identity
                  47
NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]
Seq. No.
                  224269
                  LIB3166-006-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263507
BLAST score
                  444
E value
                  3.0e-44
Match length
                  133
% identity
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
                  224270
Seq. No.
Seq. ID
                  LIB3166-006-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4220534
BLAST score
                  242
E value
                  2.0e-20
Match length
                  66
% identity
                  77
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  224271
                  LIB3166-006-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4093157
BLAST score
                  204
E value
                  5.0e-16
                  93
Match length
                  56
% identity
NCBI Description (AF087936) phytochrome-associated protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  224272
Seq. ID
                  LIB3166-006-P1-K1-F1
```



BLAST score 482
E value 1.0e-48
Match length 124
% identity 73
NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No. 224273
Seq. ID LIB3166-006-P1-K1-F2
Method BLASTY

Method BLASTX
NCBI GI g1742961
BLAST score 169
E value 5.0e-12
Match length 99
% identity 48

NCBI Description (X94756) cystathionine gamma-synthase [Arabidopsis

thaliana]

Seq. No. 224274

Seq. ID LIB3166-006-P1-K1-F5

Method BLASTX
NCBI GI g1263291
BLAST score 511
E value 5.0e-52
Match length 115
% identity 80

NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 224275

Seq. ID LIB3166-006-P1-K1-F6

Method BLASTX
NCBI GI g1531758
BLAST score 552
E value 4.0e-63
Match length 133
% identity 92

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No. 224276

Seq. ID LIB3166-006-P1-K1-G1

Method BLASTX
NCBI GI g3901012
BLAST score 501
E value 6.0e-51
Match length 125
% identity 73

NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus

sylvatica]

Seq. No. 224277

Seq. ID LIB3166-006-P1-K1-G2

Method BLASTX
NCBI GI g2462762
BLAST score 169
E value 2.0e-12
Match length 70
% identity 59



```
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  224278
                  LIB3166-006-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1518540
BLAST score
                  428
E value
                  2.0e-42
Match length
                  95
                  84
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                  224279
Seq. No.
Seq. ID
                  LIB3166-006-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q3668086
BLAST score
                  223
                  3.0e-18
E value
Match length
                  72
% identity
                  74
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  224280
Seq. No.
                  LIB3166-006-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2245131
                  304
BLAST score
                  7.0e-28
E value
Match length
                  125
% identity
                  50
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  224281
Seq. ID
                  LIB3166-006-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g4539348
BLAST score
                  167
E value
                  5.0e-12
Match length
                  56
% identity
                  55
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.
                  224282
Seq. ID
                  LIB3166-006-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3915023
BLAST score
                  318
E value
                  9.0e-30
Match length
                  86
                  70
% identity
NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1
                  (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
                  >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate
                  synthase [Citrus unshiu]
```

Seq. No. 224283



LIB3166-006-P1-K1-H10 Seq. ID Method BLASTX g2498731 NCBI GI BLAST score 318 E value 2.0e-29 Match length 84 68 % identity PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 NCBI Description >gi\_1362013\_pir\_\_S57611 zeta-crystallin homolog -Arabidopsis thaliana >gi\_886428\_emb\_CAA89838\_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana] Seq. No. 224284 Seq. ID LIB3166-006-P1-K1-H3 Method BLASTX NCBI GI g2443329 BLAST score 373 6.0e-36 E value 113 Match length 66 % identity NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana] 224285 Seq. No. LIB3166-006-P1-K1-H4 Seq. ID Method BLASTX NCBI GI g3668089 BLAST score 302 E value 2.0e-27 Match length 104 51 % identity NCBI Description (AC004667) unknown protein [Arabidopsis thaliana] 224286 Seq. No. Seq. ID LIB3166-006-P1-K1-H7 Method BLASTX NCBI GI q4263777 BLAST score 176 E value 8.0e-13 Match length 85 47 % identity NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi\_4510391\_gb\_AAD21479.1\_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana] Seq. No. 224287 Seq. ID LIB3166-007-P1-K1-A12 Method BLASTX NCBI GI q2497742 BLAST score 186 E value 6.0e-14 Match length 37 % identity 95

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) >gi\_995907 (U15153) nonspecific lipid transfer protein

precursor [Gossypium hirsutum]

Seq. No. 224288

Seq. No.

Seq. ID

224293

LIB3166-007-P1-K1-B11



```
LIB3166-007-P1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g116923
BLAST score
                   172
                   2.0e-12
E value
Match length
                   102
% identity
                   44
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi_111414_pir__S13520 beta-COP protein - rat
>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus
                   norvegicus]
Seq. No.
                   224289
Seq. ID
                   LIB3166-007-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q4158232
BLAST score
                   511
E value
                   4.0e-52
Match length
                   107
% identity
                   90
NCBI Description (Y18626) reversibly glycosylated polypeptide [Triticum
                   aestivum]
                   224290
Seq. No.
Seq. ID
                   LIB3166-007-P1-K1-A4
Method
                   BLASTX
NCBI GI 4
                   q4455364
BLAST score
                   304
E value
                   9.0e-28
Match length
                   107
% identity
                   54
NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis
                   thaliana]
Seq. No.
                   224291
Seq. ID
                   LIB3166-007-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q3193287
BLAST score
                   275
E value
                   2.0e-24
                   104
Match length
                   54
% identity
NCBI Description (AF069298) Arabidopsis predicted protein of unknown
                   function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]
Seq. No.
                   224292
Seq. ID
                   LIB3166-007-P1-K1-B1
                   BLASTX
Method
NCBI GI
                   q3128216
BLAST score
                   282
                   3.0e-25
E value
Match length
                   85
% identity
NCBI Description (AC004077) putative GA4 protein [Arabidopsis thaliana]
```

BLAST score

Match length

E value

163

91

3.0e-11



```
Method
                   BLASTX
NCBI GI
                   q3046703
BLAST score
                   421
E value
                   4.0e-65
Match length
                  136
% identity
NCBI Description
                  (AL021749) protein kinase ADK1-like protein [Arabidopsis
                  thaliana]
                  224294
Seq. No.
Seq. ID
                  LIB3166-007-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3219353
BLAST score
                  453
E value
                   2.0e-47
Match length
                  135
% identity
                   73
NCBI Description
                  (AF061514) manganese superoxide dismutase [Gossypium
                  hirsutum]
Seq. No.
                   224295
Seq. ID.
                  LIB3166-007-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4105696
BLAST score
                  275
E value
                   7.0e-25
Match length
                  57
                   93
% identity
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
Seq. No.
                   224296
Seq. ID
                  LIB3166-007-P1-K1-C1
Method
                  BLASTX
NCBI GI
                   g4049399
BLAST score
                  158
E value
                  1.0e-10
Match length
                  101
                   37
% identity
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]
Seq. No.
                   224297
Seq. ID
                  LIB3166-007-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3738291
BLAST score
                  241
E value
                   2.0e-20
                  95
Match length
                   46
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   224298
Seq. ID
                  LIB3166-007-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2827634
```



% identity NCBI Description (AL021636) putative protein [Arabidopsis thaliana] Seq. No. Seq. ID LIB3166-007-P1-K1-C7 Method BLASTX NCBI GI q1418331 BLAST score 195 E value 6.0e-15 Match length 102 % identity 39 NCBI Description (X95909) receptor like protein kinase [Arabidopsis thaliana] Seq. No. 224300 Seq. ID LIB3166-007-P1-K1-C8 Method BLASTX NCBI GI q115833 BLAST score 163 E value 2.0e-16 94 Match length 57 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR (CAB-10A) (LHCP) >gi\_100195\_pir\_\_S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi 170394 (M32605) a-binding protein [Lycopersicon esculentum] 224301 Seq. No. LIB3166-007-P1-K1-C9 Seq. ID Method BLASTX NCBI GI q4210451 BLAST score 163 E value 5.0e-19 Match length 71 % identity NCBI Description (AB016472) ARR2 protein [Arabidopsis thaliana] Seq. No. 224302 LIB3166-007-P1-K1-D1 Seq. ID Method BLASTX NCBI GI g120669 BLAST score 564 E value 3.0e-58Match length 113 % identity 94 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora] Seq. No. 224303

Seq. ID LIB3166-007-P1-K1-D10

Method BLASTX NCBI GI g541818 BLAST score 490 E value 1.0e-49



```
Match length
                   135
                   71
% identity
NCBI Description
                   protein kinase - common ice plant (fragment)
                   >gi 457693 emb CAA82994 (Z30333) protein kinase
                   [Mesembryanthemum crystallinum]
                   224304
Seq. No.
Seq. ID
                   LIB3166-007-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q3522945
BLAST score
                   183
E value
                   1.0e-13
Match length
                   95
% identity
                   35
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   224305
                   LIB3166-007-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2407790
BLAST score
                   414
E value
                   1.0e-40
Match length
                   115
% identity
                   18
NCBI Description (AF019910) grr1 [Glycine max]
Seq. No.
                   224306
                   LIB3166-007-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3688123
BLAST score
                   434
E value
                   5.0e-43
Match length
                   134
% identity
                   66
NCBI Description
                  (AJ006293) granule-bound starch synthase [Antirrhinum
                   majus]
                   224307
Seq. No.
Seq. ID
                   LIB3166-007-P1-K1-D6
                   BLASTX
Method
NCBI GI
                   g4107323
BLAST score
                   592
E value
                   2.0e-61
Match length
                   131
% identity
                   86
NCBI Description (AL035077) 60s ribosomal protein 110 [Schizosaccharomyces
                   pombe]
Seq. No.
                   224308
Seq. ID
                   LIB3166-007-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g464707
BLAST score
                   560
E value
                   9.0e-58
Match length
                   114
% identity
                   96
```

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal



protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)
S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)
S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A.
thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and
gb\_R30430 come from this gene. [Arabidopsis thaliana]

>gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal
protein [Arabidopsis thaliana]

224309 Seq. No. LIB3166-007-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g3128215 BLAST score 215 E value 3.0e-17113 Match length 49 % identity (AC004077) hypothetical protein [Arabidopsis thaliana] NCBI Description 224310 Seq. No. Seq. ID LIB3166-007-P1-K1-E10 BLASTX Method NCBI GI g3901014 BLAST score 235 1.0e-19 E value Match length 55 76 % identity (AJ130886) metallothionein-like protein class II [Fagus NCBI Description sylvatica] Seq. No. 224311 \* Seq. ID LIB3166-007-P1-K1-E3 Method BLASTX NCBI GI q2738949 BLAST score 488 E value 2.0e-49Match length 99 93 % identity NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa] Seq. No. 224312 Seq. ID LIB3166-007-P1-K1-E6 Method BLASTX NCBI GI g3894183 BLAST score 264

NCBI GI g3894183 BLAST score 264 E value 5.0e-23 Match length 109 % identity 31

NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

224318

LIB3166-007-P1-K1-F6



```
Seq. No.
Seq. ID
                  LIB3166-007-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q2558660
BLAST score
                  194
E value
                  8.0e-15
Match length
                  73
                  52
% identity
                  (AC002354) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224314
Seq. ID
                  LIB3166-007-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q462195
BLAST score
                  462
                  3.0e-46
E value
Match length
                  96
                  93
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
                  224315
Seq. No.
Seq. ID
                  LIB3166-007-P1-K1-F12
Method
                  BLASTX
NCBI GI
                 ~ q4098246
BLAST score
                  653
                  1.0e-68
E value
Match length
                  138
                  91
% identity
NCBI Description (U76410) homeobox 2 protein [Lycopersicon esculentum]
Seq. No.
                  224316
                  LIB3166-007-P1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4163997
BLAST score
                  385
E value
                   3.0e-47
Match length
                  140
% identity
                  72
                  (AF087483) alpha-xylosidase precursor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224317
Seq. ID
                  LIB3166-007-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g3250676
BLAST score
                  325
E value
                  1.0e-35
Match length
                  109
% identity
                   76
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
```



```
BLASTX
Method
NCBI GI
                  q2760349
                   375
BLAST score
E value
                   4.0e-36
Match length
                  122
                  13
% identity
                  (U84969) ubiquitin [Arabidopsis thaliana]
NCBI Description
                  224319
Seq. No.
                  LIB3166-007-P1-K1-F7
Seq. ID
Method
                  BLASTX
                   g3426038
NCBI GI
BLAST score
                   478
                   2.0e-49
E value
                  135
Match length
% identity
                   29
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   224320
Seq. No.
                  LIB3166-007-P1-K1-F9
Seq. ID
Method
                   BLASTX
                   g2443878
NCBI GI
                   310
BLAST score
                   2.0e-28
E value
Match length
                   119
                   57
% identity
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224321
                   LIB3166-007-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160156
BLAST score
                   477
E value
                   6.0e-52
                   138
Match length
                   75
% identity
                  (AC000132) Strong similarity to S. pombe leucyl-tRNA
NCBI Description
                   synthetase (gb Z73100). [Arabidopsis thaliana]
                   224322
Seq. No.
                   LIB3166-007-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3582342
BLAST score
                   226
                   1.0e-18
E value
Match length
                   126
% identity
                   41
                   (AC005496) putative flavonol 3-o-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   224323
Seq. No.
Seq. ID
                   LIB3166-007-P1-K1-G12
```

Method BLASTX
NCBI GI g2058313
BLAST score 271
E value 7.0e-24
Match length 65

% identity



```
% identity
                   (X97433) cinnamoyl-CoA reductase [Eucalyptus gunnii]
NCBI Description
                   224324
Seq. No.
                   LIB3166-007-P1-K1-G4
Seq. ID
                   BLASTX
Method
                   g2464855
NCBI GI
                   382
BLAST score
E value
                   2.0e-38
                   92
Match length
% identity
                   (Z99707) myb-related protein [Arabidopsis thaliana]
NCBI Description
                   224325
Seq. No.
Seq. ID
                   LIB3166-007-P1-K1-G5
Method
                   BLASTX
                   q3915037
NCBI GI
BLAST score
                   621
                   6.0e-65
E value
Match length
                   132
% identity
                   91
                   SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi_2570067_emb_CAA04512_ (AJ001071) second sucrose
                   synthase [Pisum sativum]
Seq. No.
                   224326
                   LIB3166-007-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1703446
                   379
BLAST score
E value
                    1.0e-36
Match length
                   116
                    68
% identity
NCBI Description
                   L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                   >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
                    thaliana]
Seq. No.
                    224327
                   LIB3166-007-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                    g3264767
BLAST score
                    415
E value
                    9.0e-41
Match length
                   125
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                    224328
Seq. No.
Seq. ID
                   LIB3166-007-P1-K1-H10
                   BLASTX
Method
NCBI GI
                    g3341685
BLAST score
                    205
E value
                    4.0e-16
Match length
                   102
                    49
```

31865

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. ID

Method



```
Seq. No.
                  224329
Seq. ID
                  LIB3166-007-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2224927
BLAST score
                  320
E value
                  4.0e-49
Match length
                  122
% identity
                  80
NCBI Description
                  (AF004213) ethylene-insensitive3-like1 [Arabidopsis
                  thaliana]
                  224330
Seq. No.
Seq. ID
                  LIB3166-007-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2495365
BLAST score
                  399
                  5.0e-39
E value
Match length
                  112
% identity
                  73
NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B
                  heat shock protein HSP81-2 [Arabidopsis thaliana]
Seq. No.
                  224331
                  LIB3166-007-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539292
BLAST score
                  475
                  7.0e-48
E value
Match length
                  103
% identity
                  84
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis
                  thaliana]
Seq. No.
                  224332
Seq. ID
                  LIB3166-007-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2618721
BLAST score
                  150
E value
                  3.0e-10
Match length
                  41
% identity
                  76
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
Seq. No.
                  224333
Seq. ID
                  LIB3166-008-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1621268
                  268
BLAST score
E value
                  9.0e-24
                  93
Match length
% identity
                  63
NCBI Description (Z81012) unknown [Ricinus communis]
                  224334
Seq. No.
```

31866

LIB3166-008-P1-K1-A12

BLASTX



```
NCBI GI
                  q3281861
BLAST score
                  375
                  4.0e-36
E value
Match length
                  127
                  56
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                  224335
Seq. No.
Seq. ID
                  LIB3166-008-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q3236253
BLAST score
                  569
                  7.0e-59
E value
Match length
                  129
% identity
                  81
NCBI Description
                  (AC004684) receptor-like protein kinase [Arabidopsis
                  thaliana]
                  224336
Seq. No.
Seq. ID
                  LIB3166-008-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4234941
BLAST score
                  227
E value
                  3.0e-19
Match length
                  52
% identity
                  87
                  (AF097938) cytosolic phosphoglucomutase [Populus tremula x
NCBI Description
                  Populus tremuloides]
                  224337
Seq. No.
Seq. ID
                  LIB3166-008-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1750376
BLAST score
                  531
E value
                  2.0e-54
Match length
                  119
% identity
                  83
                  (U80808) ubiquitin activating enzyme [Arabidopsis thaliana]
NCBI Description
                  >gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1)
                   [Arabidopsis thaliana]
                  224338
Seq. No.
                  LIB3166-008-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2979548
BLAST score
                  202
E value
                  5.0e-16
                  97
Match length
                  39
% identity
NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase
                  [Arabidopsis thaliana]
                  224339
```

Seq. No.

Seq. ID LIB3166-008-P1-K1-B3

Method BLASTX NCBI GI q478713 BLAST score 414

NCBI Description



```
1.0e-40
  E value
 Match length
                    84
                    96
  % identity
  NCBI Description
                    AP1 protein - Arabidopsis thaliana >gi 383297 prf 1902329A
                    APETALA1 gene [Arabidopsis thaliana]
  Seq. No.
                    224340
                    LIB3166-008-P1-K1-B4
  Seq. ID
 Method
                    BLASTX
                    g2618691
 NCBI GI
 BLAST score
                    179
                    4.0e-13
 E value
 Match length
                    75
                    55
  % identity
                    (AC002510) putative chloroplast envelope Ca2+-ATPase
 NCBI Description
                    [Arabidopsis thaliana]
                    224341
  Seq. No.
                    LIB3166-008-P1-K1-B7
  Seq. ID
 Method
                    BLASTX
                    g4510375
 NCBI GI
 BLAST score
                    182
 E value
                    8.0e-14
 Match length
                    72
  % identity
                    58
 NCBI Description
                    (AC007017) putative homeotic protein BEL1 [Arabidopsis
                    thaliana]
                    224342
  Seq. No.
                    LIB3166-008-P1-K1-C10
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2959781
  BLAST score
                    480
                    2.0e-48
  E value
  Match length
                    106
  % identity
  NCBI Description
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
  Seq. No.
                    224343
  Seq. ID
                    LIB3166-008-P1-K1-C3
  Method
                    BLASTX
  NCBI GI
                    g3927836
  BLAST score
                    341
                    4.0e-32
  E value
 Match length
                    114
  % identity
                    62
 NCBI Description
                   (AC005727) unknown protein [Arabidopsis thaliana]
  Seq. No.
                    224344
  Seq. ID
                    LIB3166-008-P1-K1-C4
  Method
                    BLASTX
  NCBI GI
                    g4220480
                    279
  BLAST score
# E value
                    8.0e-25
  Match length
                    119
  % identity
                    50
```

(AC006069) unknown protein [Arabidopsis thaliana]

Method

NCBI GI

E value

BLAST score

Match length

BLASTX

163

77

g2443881

3.0e-11



```
Seq. No.
                   224345
Seq. ID
                   LIB3166-008-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g2833386
BLAST score
                   275
E value
                   2.0e-24
Match length
                   81
% identity
                   74
NCBI Description
                   RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR
                   (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E)
                   >gi_2129493_pir__S62724 ribulose-phosphate 3-epimerase (EC
                   5.1.3.1) precursor - spinach >gi_1162980 (L42328)
                   ribulose-5-phosphate 3-epimerase [Spinacia oleracea]
                   >gi 3264788 (AF070941) ribulose-phosphate 3-epimerase
                   [Spinacia oleracea] >gi_1587969_prf_2207382A
D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]
Seq. No.
                   224346
                   LIB3166-008-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3367568
BLAST score
                   429
E value
                   2.0e-42
Match length
                   117
% identity
                   70
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   224347
Seq. No.
                   LIB3166-008-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3378430
BLAST score
                   188
E value
                   1.0e-14
                   61
Match length
% identity
                   66
                  (AF079317) semialdehyde dehydrogenase [Sphingomonas
NCBI Description
                   aromaticivorans]
                   224348
Seq. No.
Seq. ID
                   LIB3166-008-P1-K1-D11
                   BLASTX
Method
NCBI GI
                   g2463569
BLAST score
                   343
                   2.0e-32
E value
                   73
Match length
% identity
NCBI Description (AB007503) squalene synthase [Glycine max]
                   224349
Seq. No.
                   LIB3166-008-P1-K1-D12
Seq. ID
```

Seq. No.

224355



```
% identity
                   (ACO02294) contains beta-transducin motif [Arabidopsis
NCBI Description
                  thaliana]
                  224350
Seq. No.
                  LIB3166-008-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  g2911043
NCBI GI
BLAST score
                  234
                  1.0e-19
E value
                  106
Match length
                  53
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                  224351
Seq. No.
                  LIB3166-008-P1-K1-D5
Seq. ID
                  BLASTX
Method
                  g3582333
NCBI GI
BLAST score
                  587
E value
                   6.0e-61
Match length
                  131
                   79
% identity
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224352
                   LIB3166-008-P1-K1-D6
Seq. ID
Method
                   BLASTX
                   q3986750
NCBI GI
                   226
BLAST score
                   8.0e-19
E value
Match length
                   50
                   86
% identity
                  (AF107464) serine/threonine protein phosphatase type 2A
NCBI Description
                   [Hevea brasiliensis]
Seq. No.
                   224353
                   LIB3166-008-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4574320
BLAST score
                   106
E value
                   1.0e-08
Match length
                   59
% identity
                   63
                  (AF117224) wound-induced protein WI12 [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   224354
                   LIB3166-008-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   q4510376
NCBI GI
BLAST score
                   331
                   6.0e-31
E value
                   122
Match length
                   54
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
```

NCBI GI

BLAST score

g417073

472



```
LIB3166-008-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129915
BLAST score
                   330
E value
                   8.0e-31
Match length
                  115
                   57
% identity
                  ferredoxin precursor - sweet orange
NCBI Description
                   >gi 1360725 emb CAA87068 (Z46944) non-photosynthetic
                   ferredoxin [Citrus sinensis]
                   224356
Seq. No.
Seq. ID
                  LIB3166-008-P1-K1-F11
Method
                  BLASTX
NCBI GI
                   g2501850
BLAST score
                   507
E value
                   1.0e-51
Match length
                   102
                   92
% identity
                  (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
NCBI Description
Seq. No.
                   224357
                  LIB3166-008-P1-K1-F3
Seq. ID
Method
                  BLASTX
                   g3033400
NCBI GI
BLAST score
                   284
E value
                   7.0e-26
Match length
                   91
                   69
% identity
NCBI Description
                   (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   224358
                   LIB3166-008-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2809246
BLAST score
                   203
                   6.0e-16
E value
Match length
                   64
                   55
% identity
NCBI Description
                  (AC002560) F2401.15 [Arabidopsis thaliana]
Seq. No.
                   224359
Seq. ID
                   LIB3166-008-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g4432842
BLAST score
                   204
E value
                   5.0e-16
Match length
                   135
% identity
NCBI Description
                  (AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   224360
                   LIB3166-008-P1-K1-F7
Seq. ID
Method
                   BLASTX
```



```
2.0e-47
E value
                  118
Match length
                  75
% identity
                  GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
NCBI Description
                  >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC
                  1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate
                  synthase [Medicago sativa]
                  224361
Seq. No.
                  LIB3166-008-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g417073
NCBI GI
                  140
BLAST score
                  4.0e-09
E value
                  39
Match length
                   64
% identity
                  GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)
NCBI Description
                  >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC
                   1.4.1.14) - alfalfa >gi 166412 (L01660) NADH-glutamate
                  synthase [Medicago sativa]
                  224362
Seq. No.
                  LIB3166-008-P1-K1-G12
Seq. ID
                  BLASTX
Method
                  g1168734
NCBI GI
                   258
BLAST score
                   7.0e-31
E value
                   106
Match length
                   71
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE (CAD)
NCBI Description
                   >gi 288753_emb_CAA79622_ (Z19568) cinnamyl alcohol
                   dehydrogenase [Populus deltoides]
                   224363
Seq. No.
                   LIB3166-008-P1-K1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3142300
BLAST score
                   508
                   1.0e-51
E value
                   121
Match length
                   81
% identity
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                   protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
                   and gb_T88158, gb_N38703 and gb_AA651043 come from this
                   gene. [Arabidopsis thaliana]
                   224364
Seq. No.
Seq. ID
                   LIB3166-008-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q4376592
                   163
BLAST score
```

3.0e-11 E value Match length 121 % identity

(AE001616) S1 Ribosomal Protein [Chlamydia pneumoniae] NCBI Description

Seq. No. 224365

NCBI GI

BLAST score



```
LIB3166-008-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2224733
BLAST score
                  171
                  4.0e-12
E value
Match length
                  91
% identity
                  51
NCBI Description (AB004933) Aux22e [Vigna radiata]
Seq. No.
                  224366
                  LIB3166-008-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  279
E value
                  8.0e-31
Match length
                  104
% identity
                  70
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  224367
                  LIB3166-008-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220538
BLAST score
                  416
E value
                  5.0e-41
Match length
                  101
% identity
                  80
NCBI Description (AL035356) NADPH-ferrihemoprotein reductase ATR1
                  [Arabidopsis thaliana]
                  224368
Seq. No.
                  LIB3166-008-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580460
BLAST score
                  431
E value
                  1.0e-42
Match length
                  114
                  79
% identity
NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                  thaliana]
                  224369
Seq. No.
Seq. ID
                  LIB3166-008-P1-K1-H2
                  BLASTX
Method
NCBI GI
                  g3549667
BLAST score
                  554
                   4.0e-57
E value
                  121
Match length
                  87
% identity
NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2
                   [Arabidopsis thaliana]
                  224370
Seq. No.
Seq. ID
                  LIB3166-008-P1-K1-H9
Method
                  BLASTX
```

31873

g1657382



```
E value
                  4.0e-52
Match length
                  117
                  86
% identity
                  (Y09101) cholinephosphate cytidylyltransferase [Pisum
NCBI Description
                  sativum]
                  224371
Seq. No.
                  LIB3166-009-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119278
BLAST score
                  622
E value
                  5.0e-65
Match length
                  141
                  87
% identity
NCBI Description
                 tubulin beta-1 chain - rice
                  224372
Seq. No.
                  LIB3166-009-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462147
BLAST score
                  258
E value
                  2.0e-22
Match length
                  71
                  69
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase
                   (EC 5.3.1.9) - Arabidopsis thaliana
                  >gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate
                  isomerase [Arabidopsis thaliana]
                  224373
Seq. No.
                  LIB3166-009-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2252839
BLAST score
                  447
E value
                  2.0e-44
Match length
                  142
% identity
                  59
                  (AF013293) Similar to receptor-like protein kinase precusor
NCBI Description
                   [Arabidopsis thaliana]
                  224374
Seq. No.
                  LIB3166-009-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421941
BLAST score
                  326
                   3.0e-30
E value
                  70
Match length
                   90
% identity
                  GTP-binding protein, ras-related - common tobacco
NCBI Description
                  >gi 296878 emb CAA50609 (X71609) ras-related GTP-binding
```

protein [Nicotiana tabacum]

Seq. No. 224375

Seq. ID LIB3166-009-P1-K1-B6

Method BLASTX



```
NCBI GI
                    q115833
BLAST score
                    529
                    4.0e-54
E value
Match length
                    129
                    78
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
                    (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                    a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                    a-binding protein [Lycopersicon esculentum]
Seq. No.
                    224376
Seq. ID
                    LIB3166-009-P1-K1-C1
Method
                    BLASTX
NCBI GI
                    q1702983
BLAST score
                    325
                    3.0e-30
E value
Match length
                    110
% identity
                    56
                   AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir__S11850
NCBI Description
                    hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein
                    [Fragaria ananassa]
                 * 224377
Seq. No.
Seq. ID
                    LIB3166-009-P1-K1-C11
Method
                    BLASTX
NCBI GI
                    q3395427
BLAST score
                    169
                    6.0e-12
E value
Match length
                    103
% identity
                    36
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                    224378
Seq. ID
                    LIB3166-009-P1-K1-C3
Method
                    BLASTX
NCBI GI
                    g1943751
BLAST score
                    624
E value
                    3.0e-65
Match length
                    141
% identity
                    89
                   (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                    protein, complete sequence >gi 2078292 (U96455) ER-type
                    Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                    224379
Seq. No.
Seq. ID
                    LIB3166-009-P1-K1-C6
                    BLASTX
Method
NCBI GI
                    g2245066
```

Method BLASTX
NCBI GI g2245066
BLAST score 402
E value 3.0e-39
Match length 134
% identity 62

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 224380

Match length

% identity

120

55



```
LIB3166-009-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3608137
BLAST score
                   182
                   2.0e-13
E value
                  79
Match length
                   49
% identity
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224381
                  LIB3166-009-P1-K1-D2
Seq. ID
Method
                  BLASTX
                   g2632254
NCBI GI
BLAST score
                   371
E value
                   1.0e-35
                   102
Match length
                   70
% identity
                  (Y12465) serine/threonine kinase [Sorghum bicolor]
NCBI Description
Seq. No.
                   224382
                  LIB3166-009-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1944216
BLAST score
                   275
                   7.0e-25
E value
Match length
                   97
                   67
% identity
                  (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
NCBI Description
                   224383
Seq. No.
Seq. ID
                   LIB3166-009-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g541847
BLAST score
                   542
E value
                   1.0e-55
Match length
                   120
% identity
                   84
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
                   224384
Seq. No.
                   LIB3166-009-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   g1403522
NCBI GI
BLAST score
                   336
                   2.0e-31
E value
Match length
                   107
% identity
                   62
NCBI Description (X57187) chitinase [Phaseolus vulgaris]
                   224385
Seq. No.
Seq. ID
                   LIB3166-009-P1-K1-E2
                   BLASTX
Method
                   g4490297
NCBI GI
BLAST score
                   279
E value
                   8.0e-25
```



```
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  224386
Seq. No.
Seq. ID
                  LIB3166-009-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3287691
                  318
BLAST score
E value
                  2.0e-29
                  126
Match length
                  54
% identity
                  (AC003979) Contains similarity to RING zinc finger protein
NCBI Description
                  gb X95455 from Gallus gallus. [Arabidopsis thaliana]
                  224387
Seq. No.
                  LIB3166-009-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1871192
BLAST score
                  344
                  2.0e-32
E value
                  137
Match length
                  57
% identity
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  224388
Seq. No.
                  LIB3166-009-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g2708750
NCBI GI
                  382
BLAST score
                  7.0e-37
E value
Match length
                  134
% identity
                  56
                  (AC003952) putative physical impedence protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224389
Seq. ID
                  LIB3166-009-P1-K1-E7
                  BLASTX
Method
NCBI GI
                  q115833
BLAST score
                  412
                  2.0e-40
E value
Match length
                  108
                  75
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
                   (CAB-10A) (LHCP) >gi 100195 pir_S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi 170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                  224390
Seq. No.
                  LIB3166-009-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4545262
BLAST score
                  215
E value
                  3:0e-17
                  48
Match length
                  85
% identity
```

NCBI Description (AF118230) metallothionein-like protein [Gossypium



## hirsutum]

```
224391
Seq. No.
                  LIB3166-009-P1-K1-F12
Seq. ID
                  BLASTX
Method
                  g4099482
NCBI GI
                  266
BLAST score
                  3.0e-23
E value
                  127
Match length
                  46
% identity
                  (U87791) eRFS [Homo sapiens]
NCBI Description
                  224392
Seq. No.
                  LIB3166-009-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g541847
NCBI GI
BLAST score
                  268
                  7.0e-24
E value
                  63
Match length
                  76
% identity
                  alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
NCBI Description
                  224393
Seq. No.
                  LIB3166-009-P1-K1-F3
Seq. ID
                  BLASTX
Method
                  g1707944
NCBI GI
                   635
BLAST score
E value
                  1.0e-66
                  137
Match length
                   93
% identity
                  GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
NCBI Description
                   PRECURSOR 2 (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                   PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                   ADENYL TRANSFERASE) >gi_541976_pir__S41292
                   glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                   fava bean >gi_440595_emb_CAA54260_ (X76941) ADP-glucose
                   pyrophosphorylase [Vicia faba]
                   224394
Seq. No.
                   LIB3166-009-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4335750
                   164
BLAST score
                   7.0e-12
E value
                   57
Match length
                   58
% identity
                   (AC006284) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
                   224395
Seq. No.
Seq. ID
                   LIB3166-009-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g3023536
BLAST score
                   388
                   1.0e-37
E value
```

31878

127

58

Match length % identity



NCBI Description MADS BOX PROTEIN CMB1 >gi\_695317 (L40404) MADS box protein [Dianthus caryophyllus]

Seq. No. 224396

Seq. ID LIB3166-009-P1-K1-F9

Method BLASTX
NCBI GI g1345698
BLAST score 715
E value 6.0e-76
Match length 135
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR

(CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll

a/b-binding protein - upland cotton

>gi 452314\_emb\_CAA38025 (X54090) chlorophyll ab binding

protein [Gossypium hirsutum]

Seq. No. 224397

Seq. ID LIB3166-009-P1-K1-G10

Method BLASTX
NCBI GI g464707
BLAST score 535
E value 6.0e-55
Match length 114
% identity 90

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi\_480908\_pir\_\_S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 224398

Seq. ID LIB3166-009-P1-K1-G11

Method BLASTX
NCBI GI g3176726
BLAST score 409
E value 4.0e-44
Match length 124

NCBI Description (AC002392) putative serine proteinase [Arabidopsis

thaliana]

Seq. No. 224399

% identity

Seq. ID LIB3166-009-P1-K1-G2

Method BLASTX
NCBI GI g2244749
BLAST score 616



```
3.0e-64
E value
Match length
                    128
                    91
% identity
NCBI Description
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                    224400
Seq. ID
                   LIB3166-009-P1-K1-G3
Method
                   BLASTX
NCBI GI
                    g2109293
BLAST score
                    509
E value
                    9.0e-52
Match length
                   121
                    85
% identity
NCBI Description
                   (U97568) serine/threonine protein kinase [Arabidopsis
                    thaliana]
                    224401
Seq. No.
Seq. ID
                   LIB3166-009-P1-K1-G4
Method
                   BLASTX
NCBI GI
                    g1708236
BLAST score
                   476
E value
                    5.0e-48
Match length
                   118
                    78
% identity
NCBI Description
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
                    (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                    >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana
                    >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                    >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA
                    synthase [Arabidopsis thaliana]
                    224402
Seq. No.
Seq. ID
                   LIB3166-009-P1-K1-G5
Method
                   BLASTX
NCBI GI
                    q3334659
BLAST score
                   309
E value
                   2.0e-28
Match length
                   134
                    52
% identity
NCBI Description (Y10489) putative cytochrome P450 [Glycine max]
Seq. No.
                    224403
Seq. ID
                   LIB3166-009-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q3763933
BLAST score
                    277
E value
                   1.0e-24
```

127 Match length

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 224404

% identity

Seq. ID LIB3166-009-P1-K1-H6

Method BLASTX NCBI GI q441457

NCBI Description



```
BLAST score
                  3.0e-46
E value
Match length
                  92
% identity
                  93
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  224405
Seq. No.
                  LIB3166-009-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1946267
BLAST score
                  211
                  8.0e-17
E value
                  60
Match length
                  65
% identity
NCBI Description
                  (Y11415) myb [Oryza sativa]
                  224406
Seq. No.
                  LIB3166-010-P1-K1-A1
Seq. ID
Method
                  BLASTX
                  g2827002
NCBI GI
BLAST score
                  220
E value
                  2.0e-18
                  42
Match length
                  100
% identity
                  (AF005993) HSP70 [Triticum aestivum]
NCBI Description
                  224407
Seq. No.
                  LIB3166-010-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4580392
BLAST score
                   283
                   3.0e-25
E value
Match length
                   123
                   46
% identity
                  (AC007171) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   224408
Seq. No.
                   LIB3166-010-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1399917
BLAST score
                   156
E value
                   2.0e-10
Match length
                   79
% identity
                   41
NCBI Description
                  (U60144) replication factor C large subunit [Anas
                   platyrhynchos]
                   224409
Seq. No.
                   LIB3166-010-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1944216
                   329
BLAST score
                   3.0e - 31
E value
                   72
Match length
% identity
```

(D84246) alcohol dehydrogenase [Arabidopsis thaliana]



```
224410
Seq. No.
                   LIB3166-010-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   g1169586
NCBI GI
                   213
BLAST score
                   1.0e-17
E value
                   61
Match length
                   70
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   (CY-F1) >gi_542079_pir__S41287 fructose-bisphosphatase (EC 3.1.3.11) - potato >gi_440591_emb_CAA54265_ (X76946)
                   fructose-1,6-bisphosphatase [Solanum tuberosum]
                   224411
Seq. No.
                   LIB3166-010-P1-K1-A9
Seq. ID
                   BLASTX
Method
                   g289920
NCBI GI
                   373
BLAST score
                   4.0e-36
E value
                   89
Match length
                   82
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   224412
Seq. No.
                   LIB3166-010-P1-K1-B10
Seq. ID
                   BLASTX
Method
                   g19464
NCBI GI
                   329
BLAST score
                   1.0e-30
E value
                   85
Match length
                   62
% identity
NCBI Description (X54464) ribulose bisphosphate carboxylase [Larix
                   laricina]
                    224413
Seq. No.
                   LIB3166-010-P1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                    q231806
BLAST score
                    267
                    2.0e-36
E value
Match length
                    102
% identity
                    83
                   CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE)
NCBI Description
                    >gi_322681_pir__S29556 naringenin-chalcone synthase (EC
                    2.3.1.74) - apple tree (fragment) >gi_19589_emb_CAA48773_
                    (X68977) naregenin-chalcone synthase [Malus sp.]
                    224414
Seq. No.
                    LIB3166-010-P1-K1-B2
Seq. ID
```

Method BLASTX g1173256 NCBI GI 298 BLAST score 2.0e-27 E value Match length 68



```
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
Seq. No.
                  224415
Seq. ID
                  LIB3166-010-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g218179
BLAST score
                  183
E value
                  7.0e-21
Match length
                  92
% identity
                  59
NCBI Description (D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H
                  ATPase [Oryza sativa]
Seq. No.
                  224416
Seq. ID
                  LIB3166-010-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2129655
BLAST score
                  192
E value
                  1.0e-14
Match length
                  71
% identity
                  58
NCBI Description OBP32pep protein - Arabidopsis thaliana (fragment)
                  >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]
Seq. No.
                  224417
Seq. ID
                  LIB3166-010-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3955021
BLAST score
                  381
E value
                  1.0e-36
Match length
                  103
% identity
                  73
                  (AJ010811) HB2 homeodomain protein [Populus tremula x
NCBI Description
                  Populus tremuloides]
Seq. No.
                  224418
Seq. ID
                  LIB3166-010-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g125578
BLAST score
                  562
E value
                  5.0e-58
Match length
                  116
% identity
                  93
NCBI Description
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                   (PRK) >gi 167266 (M73707) phosphoribulokinase
                  [Mesembryanthemum crystallinum]
Seq. No.
                  224419
Seq. ID
                  LIB3166-010-P1-K1-C11
```

Mothod DIRGEN

Method BLASTX
NCBI GI g4558547
BLAST score 277
E value 1.0e-24



```
Match length
                  141
% identity
NCBI Description
                  (AC007138) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  224420
                  LIB3166-010-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3834303
BLAST score
                  428
E value
                  3.0e-42
Match length
                  138
                  63
% identity
NCBI Description (AC005679) F9K20.3 [Arabidopsis thaliana]
Seq. No.
                  224421
                  LIB3166-010-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q543905
BLAST score
                  500
E value
                  1.0e-50
Match length
                  107
% identity
                  86
                 BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
NCBI Description
                  brassinosteroid-regulated protein [Glycine max]
                  224422
Seq. No.
                  LIB3166-010-P1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3482973
BLAST score
                  429
                  2.0e-42
E value
Match length
                  127
                  71
% identity
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
Seq. No.
                  224423
Seq. ID
                  LIB3166-010-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q2980773
BLAST score
                  234
E value
                  1.0e-19
Match length
                  79
% identity
                  45
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
Seq. No.
                  224424
                  LIB3166-010-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220533
BLAST score
                  378
                  2.0e-36
E value
Match length
                  127
% identity
                  34
NCBI Description
                 (AL035356) putative mitochondrial uncoupling protein
```

Seq. No. 224425

31884

[Arabidopsis thaliana]



```
Seq. ID
                  LIB3166-010-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4454009
BLAST score
                  154
E value
                  4.0e-10
Match length
                  95
                  40
% identity
NCBI Description
                  (AL035396) putative protein [Arabidopsis thaliana]
                  224426
Seq. No.
                  LIB3166-010-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1621268
BLAST score
                  250
                  1.0e-21
E value
Match length
                  85
% identity
                  64
                  (Z81012) unknown [Ricinus communis]
NCBI Description
                  224427
Seq. No.
Seq. ID
                  LIB3166-010-P1-K1-D9
                  BLASTX
Method
NCBI GI
                  q2982251
BLAST score
                  290
                  4.0e-26
E value
                  76
Match length
% identity
                  71
                  (AF051208) putative RNA-binding protein [Picea mariana]
NCBI Description
Seq. No.
                  224428
                  LIB3166-010-P1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129825
BLAST score
                  540
E value
                  2.0e-57
Match length
                  139
% identity
                  83
NCBI Description
                  dynamin-like protein phragmoplastin 12 - soybean
                  >gi 1217994 (U25547) SDL [Glycine max]
Seq. No.
                  224429
Seq. ID
                  LIB3166-010-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  272
                  5.0e-24
E value
Match length
                  109
% identity
                  56
                  (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224430
Seq. No.
                  LIB3166-010-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1944216
BLAST score
                  358
```

31885

2.0e-34

80

E value

Match length

Seq. No.

Seq. ID

224436

LIB3166-010-P1-K1-F3



```
% identity
                  (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
NCBI Description
                  224431
Seq. No.
Seq. ID
                  LIB3166-010-P1-K1-E4
                  {\tt BLASTX}
Method
                  g1871192
NCBI GI
                  148
BLAST score
                  1.0e-09
E value
                  64
Match length
                  47
% identity
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                   224432
Seq. No.
                  LIB3166-010-P1-K1-E6
Seq. ID
                  BLASTX
Method
                  g4545262
NCBI GI
                  232
BLAST score
                  3.0e-19
E value
Match length
                   44
                   98
% identity
                  (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                  hirsutum]
                   224433
Seq. No.
                   LIB3166-010-P1-K1-E7
Seq. ID
                  BLASTX
Method
                   g4415913
NCBI GI
BLAST score
                   302
E value
                   2.0e-27
                  122
Match length
                   61
% identity
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.
                   224434
Seq. ID
                   LIB3166-010-P1-K1-F10
                   BLASTX
Method
                   q3250675
NCBI GI
BLAST score
                   253
E value
                   3.0e-22
Match length
                   75
% identity
                   67
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                   224435
                   LIB3166-010-P1-K1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3297818
BLAST score
                   373
E value
                   8.0e-36
Match length
                   104
% identity
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
```

Method

NCBI GI

BLASTX

g2935416



```
BLASTX
Method
NCBI GI
                  q4049410
                  419
BLAST score
                  3.0e-41
E value
                  118
Match length
                  66
% identity
                  (Y10225) L-ascorbate oxidase [Cucumis melo]
NCBI Description
                  224437
Seq. No.
Seq. ID
                  LIB3166-010-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g3885338
BLAST score
                  324
                  3.0e - 30
E value
                  102
Match length
                  61
% identity
                  (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224438
Seq. No.
                  LIB3166-010-P1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g116923
BLAST score
                  251
                  1.0e-21
E value
                  82
Match length
                   61
% identity
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi_111414_pir__S13520 beta-COP protein - rat
                   >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                   norvegicus]
                   224439
Seq. No.
Seq. ID
                  LIB3166-010-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q1495804
BLAST score
                   657
                   4.0e-69
E value
                   142
Match length
                   85
% identity
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.
                   224440
Seq. ID
                   LIB3166-010-P1-K1-G1
Method
                  BLASTX
NCBI GI
                   q1707955
BLAST score
                   628
E value
                   9.0e-66
Match length
                   125
                   92
% identity
NCBI Description
                  GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1
                   (GLUTAMATE--AMMONIA LIGASE) >gi 1134896 emb CAA63981
                   (X94320) glutamine synthetase [Vitis vinifera]
                   224441
Seq. No.
                  LIB3166-010-P1-K1-G10
Seq. ID
```



```
BLAST score
                  554
E value
                   5.0e-57
                  139
Match length
                  78
% identity
NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]
                  224442
Seq. No.
Seq. ID
                  LIB3166-010-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q2408068
BLAST score
                  241
                  2.0e-20
E value
Match length
                  107
                  42
% identity
NCBI Description (Z99165) hypothetical protein [Schizosaccharomyces pombe]
                  224443
Seq. No.
Seq. ID
                  LIB3166-010-P1-K1-G2
Method
                  BLASTX
                  g2370312
NCBI GI
BLAST score
                  399
                  7.0e-39
E value
                  139
Match length
                  58
% identity
NCBI Description (AJ000995) DnaJ-like protein [Medicago sativa] >gi 3202020
                   (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]
                  224444
Seq. No.
Seq. ID
                  LIB3166-010-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q2352492
                  190
BLAST score
E value
                  1.0e-14
                  68
Match length
% identity
                  59
                  (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
Seq. No.
                   224445
Seq. ID
                  LIB3166-010-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q4417267
BLAST score
                  261
E value
                  1.0e-22
Match length
                  132
                   39
% identity
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   224446
                  LIB3166-010-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g116923
                  273
BLAST score
```

31888

4.0e-24

110 43

E value Match length

% identity



NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi 111414 pir S13520 beta-COP protein - rat

>gi\_55819\_emb\_CAA40505\_ (X57228) beta COP [Rattus

norvegicus]

Seq. No. 224447

Seq. ID LIB3166-010-P1-K1-H9

Method BLASTX
NCBI GI g3935176
BLAST score 173
E value 2.0e-12

Match length 71 % identity 54

NCBI Description (AC004557) F17L21.19 [Arabidopsis thaliana]

Seq. No. 224448

Seq. ID LIB3166-011-P1-K1-A1

Method BLASTX
NCBI GI g4469023
BLAST score 323
E value 6.0e-30
Match length 98
% identity 68

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 224449

Seq. ID LIB3166-011-P1-K1-A12

Method BLASTX
NCBI GI g3212869
BLAST score 495
E value 3.0e-50
Match length 120
% identity 74

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 224450

Seq. ID LIB3166-011-P1-K1-A4

Method BLASTX
NCBI GI g2632252
BLAST score 271
E value 7.0e-24
Match length 134
% identity 46

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 224451

Seq. ID LIB3166-011-P1-K1-A5

Method BLASTX
NCBI GI 94544443
BLAST score 169
E value 5.0e-12
Match length 36
% identity 92

NCBI Description (AC006592) putative mitochondrial uncoupling protein

[Arabidopsis thaliana]

Seq. No. 224452

BLAST score

209



```
Seq. ID
                  LIB3166-011-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3702332
BLAST score
                  176
E value
                  9.0e-13
                  124
Match length
                  27
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  224453
Seq. No.
                  LIB3166-011-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129769
BLAST score
                  497
                  2.0e-50
E value
                  112
Match length
                  81
% identity
                  xyloglucan endo-transglycosylase precursor - Arabidopsis
NCBI Description
                  thaliana >gi 944810 dbj BAA09783 (D63508) endo-xyloglucan
                  transferase [Arabidopsis thaliana]
                  224454
Seq. No.
                  LIB3166-011-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455214
BLAST score
                  577
                  8.0e-60
E value
Match length
                  126
                  89
% identity
NCBI Description
                  (AL035440) putative dihydrolipoamide succinyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  224455
Seq. ID
                  LIB3166-011-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2894612
BLAST score
                  485
E value
                  6.0e-49
Match length
                  112
% identity
                  79
NCBI Description
                 (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  224456
Seq. ID
                  LIB3166-011-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q485742
BLAST score
                  569
E value
                  7.0e-59
Match length
                  125
% identity
NCBI Description
                  (L32791) pyrophosphatase [Beta vulgaris]
Seq. No.
                  224457
                  LIB3166-011-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129759
```



E value 1.0e-16 Match length 79 % identity 54 UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana NCBI Description >gi 1143392\_emb\_CAA90941\_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana] Seq. No. 224458 Seq. ID LIB3166-011-P1-K1-C1 Method BLASTX NCBI GI q4539405 BLAST score 546 E value 4.0e-56 Match length 127 % identity 82 NCBI Description (AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana] Seq. No. 224459 Seq. ID LIB3166-011-P1-K1-C10 Method BLASTX NCBI GI g1871577 BLAST score 383 E value 5.0e-37 Match length 106 % identity 67 NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa] Seq. No. 224460 Seq. ID LIB3166-011-P1-K1-C11 Method BLASTX NCBI GI q322750 BLAST score 546 E value 4.0e-56 Match length 109 % identity 99 ubiquitin / ribosomal protein CEP52 - wood tobacco NCBI Description >gi\_170217 (M74100) ubiquitin fusion protein [Nicotiana sylvestris] Seq. No. 224461 Seq. ID LIB3166-011-P1-K1-C12 Method BLASTX NCBI GI q461942 BLAST score 525 E value 1.0e-53 Match length 135 % identity 74 NCBI Description DNAJ PROTEIN HOMOLOG 1 (DNAJ-1) >gi 479277 pir S33312 dnaJ protein - leek (fragment) >gi 16087 emb CAA49211 (X69436) DNA J protein [Allium porrum] >gi\_447267\_prf\_\_1914140A DnaJ

protein [Allium porrum]

224462 Seq. No.

Seq. ID LIB3166-011-P1-K1-C2

Method BLASTX NCBI GI g409756



```
146
BLAST score
E value
                  2.0e-09
                  88
Match length
% identity
                  30
NCBI Description
                  (L25643) ATP/GTP nucleotide-binding protein [Leishmania
                  infantum]
                  224463
Seq. No.
                  LIB3166-011-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1142621
BLAST score
                  165
E value
                  3.0e-16
                  73
Match length
                  67
% identity
NCBI Description
                  (U18349) phaseolin G-box binding protein PG2 [Phaseolus
                  vulgaris]
Seq. No.
                  224464
Seq. ID
                  LIB3166-011-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4262239
BLAST score
                  273
                  4.0e-24
E value
Match length
                  133
                  43
% identity
                  (AC006200) putative membrane transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224465
                  LIB3166-011-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3335060
BLAST score
                  418
E value
                  4.0e-41
Match length
                  95
% identity
                  88
NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
                  thaliana] >gi 4468989 emb CAB38303 (AL035605) plasma
                  membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.
                  224466
                  LIB3166-011-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464707
                  538
BLAST score
                  3.0e-55
E value
Match length
                  110
                  95
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
                  protein S18.A - Arabidopsis thaliana
                  >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
```

S18 ribosomal protein [Arabidopsis thaliana]

[Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)



>gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb R30430 come from this gene. [Arabidopsis thaliana] >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

```
Seq. No.
                  224467
Seq. ID
                  LIB3166-011-P1-K1-D12
Method
                  BLASTX
                  q1071913
NCBI GI
BLAST score
                  421
                  2.0e-41
E value
                  109
Match length
                  78
% identity
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
```

- spinach >gi\_1066153\_dbj\_BAA07177\_ (D37963) cysteine

synthase [Spinacia oleracea]

```
224468
Seq. No.
Seq. ID
                  LIB3166-011-P1-K1-D4
                  BLASTX
Method
NCBI GI
                  g2262170
BLAST score
                  211
                  7.0e-17
E value
                  114
Match length
                  47
% identity
```

(AC002329) predicted glycosyl hydrolase [Arabidopsis NCBI Description

thaliana]

224469 Seq. No. LIB3166-011-P1-K1-D5 Seq. ID BLASTX Method NCBI GI g4455364 BLAST score 428 3.0e-42E value Match length 121 % identity 65

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana]

Seq. No. 224470

Seq. ID LIB3166-011-P1-K1-D6

Method BLASTX NCBI GI q2500378 BLAST score 416 E value 7.0e-41Match length 83 90 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 224471

LIB3166-011-P1-K1-E10 Seq. ID

Method BLASTX NCBI GI q1174592 BLAST score 608

NCBI GI

E value

BLAST score

q3036807

324 4.0e-30



```
2.0e-63
E value
                  113
Match length
                  99
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                  - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                  sativum]
                  224472
Seq. No.
                  LIB3166-011-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g2052379
NCBI GI
BLAST score
                  169
                  3.0e-12
E value
                  35
Match length
                  86
% identity
                  (U66343) calreticulin [Arabidopsis thaliana]
NCBI Description
                  224473
Seq. No.
                  LIB3166-011-P1-K1-E2
Seq. ID
                  BLASTX
Method
                  q3080400
NCBI GI
                  302
BLAST score
                  2.0e-35
E value
                  119
Match length
                  65
% identity
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4455264 emb_CAB36800.1_ (AL035527) putative protein
                   [Arabidopsis thaliana]
                  224474
Seq. No.
Seq. ID
                  LIB3166-011-P1-K1-E3
                  BLASTX
Method
                  g2292917
NCBI GI
                   258
BLAST score
                   2.0e-22
E value
                  84
Match length
                   64
% identity
                  (X99851) galactokinase [Arabidopsis thaliana]
NCBI Description
                   224475
Seq. No.
                  LIB3166-011-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   q128194
NCBI GI
BLAST score
                   462
                   2.0e-46
E value
Match length
                   113
                   80
% identity
                  NITRATE REDUCTASE (NR) >gi 81572 pir A41667 nitrate
NCBI Description
                   reductase (NADH) (EC 1.6.6.1) - winter squash >gi 167499
                   (M33154) nitrate reductase [Cucurbita maxima]
                   224476
Seq. No.
                   LIB3166-011-P1-K1-E7
Seq. ID
Method
                   BLASTX
```



```
88
Match length
% identity
                  (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                  224477
Seq. No.
                  LIB3166-011-P1-K1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  a498038
                  282
BLAST score
                  2.0e-29
E value
                  106
Match length
                  60
% identity
                  (L33792) lipid transfer protein [Senecio odorus]
NCBI Description
                  224478
Seq. No.
                  LIB3166-011-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3298441
BLAST score
                  270
E value
                  9.0e-24
                  103
Match length
                  58
% identity
                  (AB010879) chloroplast ribosomal protein L10 [Nicotiana
NCBI Description
                  tabacum]
                  224479
Seq. No.
                  LIB3166-011-P1-K1-F12
Seq. ID
                  BLASTX
Method
                  g2982303
NCBI GI
BLAST score
                   551
                   9.0e-57
E value
                  127
Match length
                   81
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
                   224480
Seq. No.
                   LIB3166-011-P1-K1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4490736
BLAST score
                   331
                   6.0e-31
E value
Match length
                   132
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                   224481
                   LIB3166-011-P1-K1-F7
Seq. ID
Method
                   BLASTX
                   g629541
NCBI GI
BLAST score
                   484
                   8.0e-49
E value
                   115
Match length
% identity
                   81
                  plasma membrane intrinsic protein 1c - Arabidopsis thaliana
NCBI Description
                   >gi 472875 emb_CAA53476_ (X75882) plasma membrane intrinsic
```

protein 1c [Arabidopsis thaliana]



```
224482
Seq. No.
Seq. ID
                   LIB3166-011-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3341679
BLAST score
                   274
E value
                   3.0e-24
                   82
Match length
                   70
% identity
                   (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                   [Arabidopsis thaliana]
                   224483
Seq. No.
Seq. ID
                   LIB3166-011-P1-K1-F9
                   BLASTX
Method
                   g3775997
NCBI GI
                   391
BLAST score
                   6.0e-38
E value
                   90
Match length
                   84
 % identity
                   (AJ010462) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   224484
 Seq. No.
 Seq. ID
                   LIB3166-011-P1-K1-G1
                   BLASTX
Method
                   g2511541
NCBI GI
                   402
BLAST score
                   1.0e-39
E value
                   90
Match length
                   88
 % identity
                   (AF020787) DNA-binding protein GBP16 [Oryza sativa]
NCBI Description
                   224485
 Seq. No.
 Seq. ID
                   LIB3166-011-P1-K1-G12
                   BLASTX
Method
                   g3901012
 NCBI GI
                   602
 BLAST score
                   1.0e-62
 E value
                   135
 Match length
                   76
 % identity
NCBI Description
                   (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
                   sylvatica]
                   224486
 Seq. No.
 Seq. ID
                   LIB3166-011-P1-K1-G2
                   BLASTX
 Method
 NCBI GI
                   q2961372
 BLAST score
                    432
                    8.0e-43
 E value
 Match length
                    85
 % identity
                    93
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
 NCBI Description
                    thaliana] >gi 3036817 emb CAA18507_ (AL022373) ribosomal
                   protein L2 [Arabidopsis thaliana]
```

Seq. No. 224487

Seq. ID LIB3166-011-P1-K1-G3

Method BLASTX



```
q4544403
NCBI GI
 BLAST score
                    624
 E value
                    3.0e-65
                    139
 Match length
                    81
  % identity
 NCBI Description
                   (AC007047) putative glucan endo-1,3-beta-D-glucosidase
                    precursor [Arabidopsis thaliana]
 Seq. No.
                    224488
                    LIB3166-011-P1-K1-G4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1220196
 BLAST score
                    508
 E value
                    1.0e-51
 Match length
                    112
                    85
  % identity
                   (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
 NCBI Description
 Seq. No.
                    224489
 Seq. ID
                    LIB3166-011-P1-K1-G9
 Method
                    BLASTX
 NCBI GI
                    g3941543
 BLAST score
                    241
                    2.0e-20
 E value
 Match length
                    72
                    68
  % identity
                    (AF069497) pelota [Arabidopsis thaliana]
 NCBI Description
                    >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                    [Arabidopsis thaliana]
                    224490
 Seq. No.
 Seq. ID
                    LIB3166-011-P1-K1-H1
 Method
                    BLASTX
 NCBI GI
                    q3434967
 BLAST score
                    204
                    4.0e-16
 E value
 Match length
                    85
                    53
 % identity
 NCBI Description
                   (AB008103) ethylene responsive element binding factor 1
                    [Arabidopsis thaliana]
                    224491
 Seq. No.
                    LIB3166-011-P1-K1-H4
 Seq. ID
 Method
                    BLASTX
                    g2982453
 NCBI GI
 BLAST score
                    291
 E value
                    3.0e-26
                    99
 Match length
 % identity
                    62
 NCBI Description
                   (AL022223) fructose-bisphosphate aldolase-like protein
                    [Arabidopsis thaliana]
                    224492
 Seq. No.
 Seq. ID
                    LIB3166-011-P1-K1-H9
 Method
                    BLASTX
```

31897

g3885328

157

NCBI GI BLAST score



```
9.0e-11
E value
Match length
                  83
                  40
% identity
NCBI Description
                  (AC005623) putative serine/threonine protein kinase
                  [Arabidopsis thaliana]
                  224493
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-A4
Method
                  BLASTX
                  q91035
NCBI GI
                  608
BLAST score
                  2.0e-63
E value
Match length
                  127
                  93
% identity
                  laminin receptor homolog - mouse >gi 52853 emb CAA29696
NCBI Description
                   (X06406) protein p40 (AA 1 - 295) [Mus musculus]
                  >gi 228997 prf 1815216A laminin receptor [Cricetinae gen.
                  sp.]
                  224494
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-A5
                  BLASTX
Method
                  q2894106
NCBI GI
BLAST score
                  654
                  8.0e-69
E value
                  127
Match length
                  94
% identity
                  (Z78279) Collagen alpha1 [Rattus norvegicus]
NCBI Description
Seq. No.
                  224495
                  LIB3166-012-P1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3164123
BLAST score
                   643
E value
                   2.0e-67
Match length
                  126
                   94
% identity
NCBI Description
                  (AJ224880) collagen alpha 2 type V [Rattus norvegicus]
Seq. No.
                   224496
Seq. ID
                  LIB3166-012-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q127177
BLAST score
                   223
E value
                   2.0e-18
Match length
                  87
% identity
                   54
                  MYOSIN REGULATORY LIGHT CHAIN 2, SKELETAL MUSCLE ISOFORM
NCBI Description
                   (G2) (DTNB) (MLC-2) >gi_71706_pir__MORTL2 myosin L2 (DTNB)
                   regulatory light chain precursor, skeletal muscle - rat
                   >gi 825539_emb_CAA25480_ (X00975) MLC2 [Rattus norvegicus]
```

Seq. No. 224497

Seq. ID LIB3166-012-P1-K1-B10

Method BLASTX NCBI GI g309233 BLAST score 413

Match length

% identity



```
1.0e-40
E value
Match length
                  79
                  100
% identity
                  (M24509) ferritin heavy chain [Mus musculus] >gi 1435203
NCBI Description
                  (U58829) ferritin-H subunit [Rattus norvegicus]
                  224498
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-B2
                  BLASTX
Method
                  g1588365
NCBI GI
BLAST score
                  382
                  8.0e-37
E value
                  104
Match length
                  74
% identity
NCBI Description signal peptidase:SUBUNIT=12kD [Homo sapiens]
                  224499
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-B7
                  BLASTX
Method
                  g2894106
NCBI GI
                  337
BLAST score
                  4.0e-32
E value
                  66
Match length
                  98
% identity
NCBI Description (Z78279) Collagen alpha1 [Rattus norvegicus]
                  224500
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-C1
                  BLASTX
Method
NCBI GI
                  q111946
BLAST score
                  407
                  8.0e-40
E value
                  84
Match length
                  88
% identity
NCBI Description matrix Gla protein precursor - rat
                  224501
Seq. No.
                  LIB3166-012-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2135915
                  670
BLAST score
E value
                  1.0e-70
                  127
Match length
                   95
% identity
NCBI Description phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32)
                  precursor, mitochondrial - human >gi 1403050 emb CAA63380
                   (X92720) phosphoenolpyruvate carboxykinase (GTP) [Homo
                  sapiens]
                   224502
Seq. No.
                  LIB3166-012-P1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4098993
BLAST score
                   474
                  1.0e-47
E value
```



(U81491) polyhomeotic 2 [Mus musculus] NCBI Description 224503 Seq. No. Seq. ID LIB3166-012-P1-K1-C7 Method BLASTX q417192 NCBI GI 414 BLAST score E value 1.0e-40 97 Match length 78 % identity MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (MCP-3) (MONOCYTE NCBI Description CHEMOATTRACTANT PROTEIN 3) (INTERCRINE/CHEMOKINE MARC) (FIC PROTEIN) >qi 57938 emb CAA78169 (Z12297) intercrine [Mus musculus] >gi 547089 bbs 149941 (S71251) monocyte chemotactic protein-3, MCP-3, Marc/Fic protein [mice, macrophage cell line WEHI-3, Peptide, 97 aa] [Mus sp.] Seq. No. 224504 Seq. ID LIB3166-012-P1-K1-E11 Method BLASTX q123651 NCBI GI 506 BLAST score 5.0e-62 E value 134 Match length 96 % identity HEAT SHOCK COGNATE 71 KD PROTEIN >gi 111759 pir S07197 NCBI Description heat shock cognate protein hsc73 - rat >gi\_2119718\_pir\_\_JC4853 heat-shock protein 73 - mouse >qi 56379 emb CAA68265 (Y00054) hsc73 [Rattus norvegicus] >qi 204667 (M11942) 70 kDa heat-shock-like protein [Rattus norvegicus] >gi 861213 (U27129) heat shock 73 protein [Mus musculus] 224505 Seq. No. Seq. ID LIB3166-012-P1-K1-E12 BLASTX Method NCBI GI q3043917 BLAST score 345 1.0e-32 E value Match length 113 63 % identity (AF029844) elongation factor 1-beta homolog [Mus musculus] NCBI Description 224506 Seq. No. LIB3166-012-P1-K1-E6 Seq. ID BLASTX Method g114291 NCBI GI 272 BLAST score 1.0e-24 E value Match length 53 98 % identity ARGININOSUCCINATE SYNTHASE (CITRULLINE--ASPARTATE LIGASE) NCBI Description

>gi 68637 pir AJRTRS argininosuccinate synthase (EC

6.3.4.5) - rat >gi\_55767\_emb\_CAA30999\_ (X12459)

argininosuccinate synthetase  $\overline{(AA 1-41\overline{2})}$  [Rattus norvegicus] >gi\_203016 (M36708) argininosuccinate synthetase [Rattus

norvegicus]

E value

Match length

1.0e-19



```
224507
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-F10
                  BLASTX
Method
                  g137475
NCBI GI
BLAST score
                  729
                  1.0e-77
E value
                  139
Match length
                  99
% identity
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                  (32 KD ACCESSORY PROTEIN) (P39) >gi 89602 pir A32123
                  H+-transporting ATPase (EC 3.6.1.35) polypeptide IV,
                  vacuolar - bovine
                  224508
Seq. No.
                  LIB3166-012-P1-K1-F11
Seq. ID
                  BLASTX
Method
                  g2833633
NCBI GI
                  611
BLAST score
E value
                  1.0e-63
Match length
                  136
% identity
                  81
NCBI Description (AC003108) Unknown gene product [Homo sapiens]
                  224509
Seq. No.
                  LIB3166-012-P1-K1-F12
Seq. ID
                 BLASTX
Method
                  g543201
NCBI GI
                  611
BLAST score
                  1.0e-63
E value
Match length
                  132
% identity
                 84
NCBI Description collagen alpha 1(I) chain precursor - mouse (fragments)
                  224510
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-F3
                  BLASTX
Method
                  g117505
NCBI GI
                  193
BLAST score
E value
                  6.0e-15
                  71
Match length
% identity
NCBI Description CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
                  (CALBP) (CALCIUM-BINDING PROTEIN 3) (CABP3)
                  >qi 627974 pir JH0819 calreticulin precursor - rat
                  >gi 55855 emb CAA37446 (X53363) precursor (AA -17 to 399)
                   [Rattus norvegicus] >gi 488841 emb CAA55890 (X79327)
                  calreticulin [Rattus norvegicus] >gi 1845572 dbj BAA11345
                   (D78308) calreticulin [Rattus norvegicus]
Seq. No.
                  224511
                  LIB3166-012-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g478811
BLAST score
                  232
```



```
% identity
NCBI Description
                  polyubiquitin - bovine >gi_645_emb_CAA79146_ (Z18245)
                  polyubiquitin [Bos taurus]
                  224512
Seq. No.
                  LIB3166-012-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2961553
BLAST score
                  559
E value
                  9.0e-58
                  113
Match length
                  100
% identity
                  (AF049878) amyloid beta-peptide binding protein; ERAB
NCBI Description
                  [Rattus norvegicus]
                  224513
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q231671
BLAST score
                  156
E value
                  2.0e-10
                  31
Match length
                  94
% identity
                  PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR
NCBI Description
                  >gi 284994 pir A43291 collagen alpha 2(I) chain precursor
                  - mouse >gi 50489 emb CAA41205 (X58251) pro-alpha-2(I)
                  collagen [Mus musculus]
Seq. No.
                  224514
Seq. ID
                  LIB3166-012-P1-K1-G8
Method
                  BLASTX
                  g119146
NCBI GI
BLAST score
                  628
                  6.0e-68
E value
Match length
                  135
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
                  FACTOR TU) (EF-TU) >gi_90198_pir__JU0133 translation
                  elongation factor eEF-1 alpha chain - Chinese hamster
                  >gi_111601_pir__S21055 translation elongation factor eEF-1
                  alpha chain - rat >gi 56080 emb CAA43378 (X61043)
                  elongation factor 1 alpha [Rattus norvegicus]
                  >gi 56093 emb CAA45122 (X63561) elongation factor 1-alpha
                  [Rattus norvegicus] >gi 220279 dbj BAA00409 (D00522) EF-1
```

alpha [Cricetulus longicaudatus]

Seq. No. 224515

LIB3166-012-P1-K1-H12 Seq. ID

Method BLASTX NCBI GI g3123887 BLAST score 267 1.0e-23 E value Match length 63 % identity 81

(AF027706) serine/threonine kinase RICK [Homo sapiens] NCBI Description >gi 3264574 (AC004003) serine/threonine kinase RICK; match

to protein AF027706 (PID:g3123887) and mRNA AF027706



(NID:g3123886) [Homo sapiens] >gi\_3290172 (AF064824) CARD-containing ICE associated kinase [Homo sapiens] >gi\_3342910 (AF078530) receptor interacting protein 2 [Homo sapiens] >gi\_4151948 (AF117829) serine/threonine kinase RICK [Homo sapiens] >gi\_4506537\_ref\_NP\_003812.1\_pRIP2\_UNKNOWN

```
224516
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-H3
                  BLASTX
Method
                  q809561
NCBI GI
                  427
BLAST score
                  3.0e-42
E value
                  87
Match length
                  95
% identity
NCBI Description (X13055) gamma-actin [Mus musculus]
                  224517
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g548747
BLAST score
                  312
                  2.0e-32
E value
                  71
Match length
                  92
% identity
                  60S RIBOSOMAL PROTEIN L13A >gi 1363320 pir A53204
NCBI Description
                  ribosomal protein L13a - rat >gi 460776_emb_CAA48343
                  (X68282) rat ribosomal protein L13a [Rattus norvegicus]
                  224518
Seq. No.
Seq. ID
                  LIB3166-012-P1-K1-H7
                  BLASTX
Method
NCBI GI
                  q1213490
                  200
BLAST score
                  3.0e-20
E value
Match length
                  56
% identity
                  95
NCBI Description (U42719) C4 complement protein [Rattus norvegicus]
Seq. No.
                  224519
                  LIB3166-012-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  q1173177
NCBI GI
BLAST score
                  471
                  1.0e-47
E value
Match length
                  93
% identity
                  96
NCBI Description
                  40S RIBOSOMAL PROTEIN S10 >gi 1362933 pir S55918 ribosomal
                  protein S10 - human >gi 550025 (U14972) ribosomal protein
                  S10 [Homo sapiens] >gi 1096944 prf 2113200G ribosomal
                  protein S10 [Homo sapiens]
                  >gi 4506679 ref NP 001005.1 pRPS10 ribosomal protein S10
```

Seq. No. 224520

Seq. ID LIB3166-013-P1-K1-A12

Method BLASTX NCBI GI g2443757

Match length

% identity



```
306
BLAST score
                  3.0e-28
E value
Match length
                  90
% identity
                  67
                  (AF020434) cyclophilin [Arabidopsis thaliana]
NCBI Description
                  224521
Seq. No.
                  LIB3166-013-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4510376
BLAST score
                  362
                  2.0e-34
E value
                  144
Match length
                  54
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224522
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-B12
                  BLASTX
Method
NCBI GI
                  g4107276
BLAST score
                  261
                  1.0e-22
E value
                  59
Match length
                  90
% identity
                 (X98506) acetyl-CoA synthetase [Solanum tuberosum]
NCBI Description
                   224523
Seq. No.
                  LIB3166-013-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3451072
BLAST score
                  240
                   2.0e-20
E value
                   72
Match length
                   58
% identity
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                   224524
Seq. No.
Seq. ID
                   LIB3166-013-P1-K1-B6
                   BLASTX
Method
NCBI GI
                   g113363
BLAST score
                   511
                   2.0e-54
E value
                   129
Match length
                   77
% identity
                  ALCOHOL DEHYDROGENASE 1 >gi 279445 pir DEPJA1 alcohol
NCBI Description
                   dehydrogenase (EC 1.1.1.1) 1 - garden petunia
                   >gi 20506 emb CAA38039 (X54106) alcohol dehydrogenase
                   [Petunia x hybrida]
                   224525
Seq. No.
                   LIB3166-013-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4314355
BLAST score
                   305
                   8.0e-28
E value
```



```
224526
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-B9
                  BLASTX
Method
                  q2522534
NCBI GI
                  185
BLAST score
                  2.0e-14
E value
Match length
                  86
                  48
% identity
                  (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]
NCBI Description
                  224527
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-C1
                  BLASTX
Method
NCBI GI
                  q3269293
BLAST score
                  276
                  1.0e-24
E value
Match length
                  103
% identity
                  57
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                  224528
Seq. No.
                  LIB3166-013-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g2961378
NCBI GI
                   574
BLAST score
                   2.0e-59
E value
                  143
Match length
                  39
% identity
NCBI Description (AL022141) putative protein [Arabidopsis thaliana]
                   224529
Seq. No.
                   LIB3166-013-P1-K1-C5
Seq. ID
Method
                   BLASTX
                   g3021489
NCBI GI
BLAST score
                   164
                   2.0e-15
E value
                   88
Match length
% identity
                   62
NCBI Description (AJ224934) histone H2B [Lycopersicon esculentum]
                   224530
Seq. No.
                   LIB3166-013-P1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3122388
BLAST score
                   610
                   1.0e-63
E value
Match length
                   131
                   31
% identity
NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi 2394231 (AF016847) WD-40
                   repeat protein [Arabidopsis thaliana]
                   224531
Seq. No.
                   LIB3166-013-P1-K1-C7
Seq. ID
Method
                   BLASTX
                   q4510345
NCBI GI
```

NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]



```
275
BLAST score
E value
                  2.0e-24
                  63
Match length
                  75
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224532
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3660552
BLAST score
                  221
E value
                  5.0e-18
                  51
Match length
                  76
% identity
                  (AB013817) DREB1C [Arabidopsis thaliana]
NCBI Description
                  >gi 3738228 dbj BAA33793 (AB007789) DREB1C [Arabidopsis
                  thaliana] >gi 3907541 (AF062925) transcriptional activator
                  CBF1 homolog [Arabidopsis thaliana]
                  >qi 4322228 gb AAD15976 (AF074601) CRT/DRE binding factor
                  2 [Arabidopsis thaliana]
                  224533
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  g3367593
BLAST score
                  251
                  2.0e-21
E value
                  120
Match length
                  58
% identity
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3805841 emb CAA21461 (AL031986) putative protein
                   [Arabidopsis thaliana]
                   224534
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-D3
                  BLASTX
Method
                  g1168734
NCBI GI
BLAST score
                   503
                   4.0e-51
E value
Match length
                   133
                   77
% identity
NCBI Description
                  CINNAMYL-ALCOHOL DEHYDROGENASE (CAD)
                   >qi 288753 emb CAA79622 (Z19568) cinnamyl alcohol
                   dehydrogenase [Populus deltoides]
Seq. No.
                   224535
                   LIB3166-013-P1-K1-E10
Seq. ID
                   BLASTX
Method
                   g3894173
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
Match length
                   32
                   75
% identity
                  (AC005312) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 224536 Seq. ID LIB3166-013-P1-K1-E11



```
Method
                  BLASTX
NCBI GI
                  g3123271
BLAST score
                  262
                  3.0e-23
E value
Match length
                  59
                  86
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S6 >qi 2224751 emb CAA74381 (Y14052)
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  224537
Seq. ID
                  LIB3166-013-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q3193292
BLAST score
                  517
                  9.0e-53
E value
Match length
                  122
% identity
                  85
NCBI Description
                  (AF069298) similar to ATPases associated with various
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                  [Arabidopsis thaliana]
                  224538
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2754746
BLAST score
                  309
                  2.0e-28
E value
Match length
                  143
% identity
                  50
NCBI Description (U85448) sucrose-phosphate synthase [Actinidia deliciosa]
Seq. No.
                  224539
                  LIB3166-013-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2736288
BLAST score
                  146
                  3.0e-09
E value
                  33
Match length
% identity
                  79
NCBI Description
                  (AF031080) isopentenyl diphosphate isomerase II
                  [Camptotheca acuminata]
                  224540
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  267
                  5.0e-24
E value
Match length
                  72
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                  224541
Seq. No.
```

Seq. ID LIB3166-013-P1-K1-F12

Method BLASTX NCBI GI g1350777 BLAST score 324



```
4.0e-30
E value
Match length
                  75
                  87
% identity
                  60S RIBOSOMAL PROTEIN L9 >gi 971282 dbj BAA07209 (D38012)
NCBI Description
                  ribosomal protein L9 [Oryza sativa]
                  224542
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-F2
Method
                  BLASTX
                  q4090533
NCBI GI
BLAST score
                  460
                  3.0e-46
E value
                  101
Match length
                  82
% identity
                 (U68215) ACC oxidase [Carica papaya]
NCBI Description
                  224543
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2146739
BLAST score
                  262
                  8.0e-23
E value
                  118
Match length
                  51
% identity
                 hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi 881521
NCBI Description
                  (U28214) hexokinase 1 [Arabidopsis thaliana]
                  224544
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q400976
                  426
BLAST score
E value
                  1.0e-48
                  108
Match length
% identity
                  96
                 RAS-RELATED PROTEIN RHA1 >gi 478671 pir S23727 GTP-binding
NCBI Description
                  protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_
                  (X59152) RHA1 [Arabidopsis thaliana]
                  >gi 397594 emb CAA80534 (Z22958) GTP-binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  224545
                  LIB3166-013-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1888357
BLAST score
                  499
E value
                  1.0e-50
Match length
                  123
% identity
                  76
NCBI Description
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
                  >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
```

precursor [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3166-013-P1-K1-G10

224546

Method BLASTX NCBI GI g2673910



```
BLAST score
E value
                  2.0e-09
                  67
Match length
                  54
% identity
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
                  224547
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-G12
Method
                  BLASTX
                  q1061420
NCBI GI
                  512
BLAST score
                  4.0e-52
E value
Match length
                  127
                  82
% identity
                 (U38965) p-type H+-ATPase [Vicia faba]
NCBI Description
                  224548
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-G2
Method
                  BLASTX
                  g3341468
NCBI GI
BLAST score
                  170
                  5.0e-12
E value
                  85
Match length
                  45
% identity
NCBI Description (AJ009594) Dof zinc finger protein [Nicotiana tabacum]
                  224549
Seq. No.
                  LIB3166-013-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1655653
BLAST score
                  113
                  6.0e-09
E value
Match length
                  100
                  38
% identity
NCBI Description (Z81368) hypothetical protein Rv2406c [Mycobacterium
                  tuberculosis]
                  224550
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3136336
                  415
BLAST score
                  6.0e-41
E value
Match length
                  81
% identity
                  52
NCBI Description (AF064552) calmodulin; Cam [Apium graveolens]
Seq. No.
                  224551
                  LIB3166-013-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2281090
BLAST score
                  394
                  3.0e-38
E value
Match length
                  115
% identity
                  65
```

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]



Seq. No.

```
Seq. ID
                  LIB3166-013-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g629722
                  175
BLAST score
                  1.0e-12
E value
                  122
Match length
                  35
% identity
                  finger protein pcp1 - potato >gi_563623 emb CAA57772
NCBI Description
                  (X82328) putative DNA/RNA binding protein [Solanum
                  tuberosum]
                  224553
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g4406787
                  388
BLAST score
                  1.0e-37
E value
                  102
Match length
                  77
% identity
                 (AC006532) NADH dehydrogenase [Arabidopsis thaliana]
NCBI Description
                  224554
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-G9
Method
                  BLASTX
                  g3892059
NCBI GI
                  270
BLAST score
                  1.0e-23
E value
                  143
Match length
                  48
% identity
                  (AC002330) predicted protein of unknown function
NCBI Description
                  [Arabidopsis thaliana]
                  224555
Seq. No.
Seq. ID
                  LIB3166-013-P1-K1-H10
                  BLASTX
Method
NCBI GI
                  g2983778
BLAST score
                  164
                  2.0e-11
E value
Match length
                  116
                  36
% identity
NCBI Description (AE000736) hypothetical protein [Aquifex aeolicus]
Seq. No.
                  224556
Seq. ID
                  LIB3166-013-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4512694
BLAST score
                  238
E value
                  6.0e-20
Match length
                  133
% identity
                  41
NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]
                  224557
Seq. No.
                  LIB3166-013-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464621
```



BLAST score 278 E value 9.0e-25 104 Match length 54 % identity 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi\_280374\_pir\_\_\_\$28586 NCBI Description ribosomal protein ML16 - common ice plant >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum] 224558 Seq. No. Seq. ID LIB3166-013-P1-K1-H9 BLASTX Method NCBI GI g3334320 BLAST score 482 1.0e-48 E value Match length 108 % identity 92 NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi\_2444420 (AF020553) ribosome-associated protein p40 [Glycine max] 224559 Seq. No. LIB3166-014-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g3540195 BLAST score 441 8.0e-44E value 135 Match length 31 % identity NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana] 224560 Seq. No. Seq. ID LIB3166-014-P1-K1-A10 Method BLASTX NCBI GI q4467147 BLAST score 194 E value 5.0e-22Match length 110 % identity 56 NCBI Description (AL035540) putative protein [Arabidopsis thaliana] Seq. No. 224561 LIB3166-014-P1-K1-A12 Seq. ID Method BLASTX NCBI GI g541546 BLAST score 306 6.0e-38 E value

Match length 110 % identity 16

ubiquitin precursor - Volvox carteri NCBI Description

>gi 395295 emb CAA52290 (X74214) polyubiquitin [Volvox

carteri]

Seq. No. 224562

LIB3166-014-P1-K1-A4 Seq. ID

BLASTX Method g2982303 NCBI GI BLAST score 574



```
E value
                  2.0e-59
Match length
                  131
                  79
% identity
                 (AF051236) hypothetical protein [Picea mariana]
NCBI Description
                  224563
Seq. No.
                  LIB3166-014-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3264767
BLAST score
                  500
                  9.0e-51
E value
                  119
Match length
                  76
% identity
NCBI Description
                 (AF071893) AP2 domain containing protein [Prunus armeniaca]
                  224564
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q4454050
BLAST score
                  301
                  2.0e-27
E value
                  79
Match length
                  66
% identity
NCBI Description (AL035394) putative protein [Arabidopsis thaliana]
                  224565
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2190419
BLAST score
                  202
                  8.0e-16
E value
                  109
Match length
                  40
% identity
NCBI Description (Y13632) dem [Lycopersicon esculentum]
                  224566
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1432056
BLAST score
                  184
E value
                  1.0e-13
Match length
                  110
                  45
% identity
NCBI Description (U56834) WRKY3 [Petroselinum crispum]
Seq. No.
                  224567
                  LIB3166-014-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2318137
BLAST score
                  590
E value
                  2.0e-61
Match length
                  117
% identity
                  97
NCBI Description
                  (AF014052) Mg protoporphyrin IX chelatase [Nicotiana
                  tabacum]
```

224568

Seq. No.

Seq. No.

Seq. ID

224573

LIB3166-014-P1-K1-C6



```
LIB3166-014-P1-K1-B6
Seq. ID
                  BLASTX
Method
                  g2970654
NCBI GI
BLAST score
                  184
                  8.0e-14
E value
Match length
                  83
                  58
% identity
                 (AF052058) ferritin subunit cowpea2 precursor [Vigna
NCBI Description
                  unguiculata]
                  224569
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-B7
                  BLASTX
Method
NCBI GI
                  g2970654
BLAST score
                  215
                  2.0e-17
E value
                  97
Match length
                  57
% identity
                  (AF052058) ferritin subunit cowpea2 precursor [Vigna
NCBI Description
                  unguiculata]
                  224570
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1814424
BLAST score
                  575
                  2.0e-59
E value
Match length
                  134
                  78
% identity
NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
                  224571
Seq. No.
                  LIB3166-014-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231675
BLAST score
                  163
                  1.0e-23
E value
Match length
                  64
                  86
% identity
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 282955 pir S23525
                  cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common
                  tobacco >qi 19839 emb CAA44216 (X62343) cinnamyl-alcohol
                  dehydrogenase [Nicotiana tabacum]
Seq. No.
                  224572
                  LIB3166-014-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204293
BLAST score
                  503
E value
                  4.0e-51
Match length
                  125
% identity
                  76
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
```



```
BLASTX
Method
NCBI GI
                  g2980770
BLAST score
                  410
                  3.0e-40
E value
Match length
                  125
                  66
% identity
                 (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  224574
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q2980770
BLAST score
                  420
E value
                  2.0e-41
Match length
                  133
                  65
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  224575
Seq. ID
                  LIB3166-014-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4512651
BLAST score
                  520
                  4.0e-53
E value
Match length
                  133
                  68
% identity
                  (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224576
                  LIB3166-014-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  q289920
NCBI GI
BLAST score
                  384
E value
                  3.0e - 37
Match length
                  102
                  75
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  224577
                  LIB3166-014-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652104
BLAST score
                  330
                  8.0e-31
E value
Match length
                  125
% identity
                  51
NCBI Description (D90902) hypothetical protein [Synechocystis sp.]
Seq. No.
                  224578
                  LIB3166-014-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129921
BLAST score
                  179
                  3.0e-13
E value
```

Match length



% identity

```
% identity
                  73
                  hypothetical protein 1 - Madagascar periwinkle >gi 758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
Seq. No.
                  224579
Seq. ID
                  LIB3166-014-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2262111
BLAST score
                  197
E value
                  3.0e-15
Match length
                  75
                  55
% identity
                  (AC002343) ribitol dehydrogenase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  224580
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-D4
                  BLASTX
Method
NCBI GI
                  q1769887
BLAST score
                  556
                  3.0e-57
E value
                  129
Match length
                  85
% identity
NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]
                  224581
Seq. No.
                  LIB3166-014-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1906828
BLAST score
                   432
E value
                   8.0e-43
Match length
                  104
% identity
                   84
NCBI Description (Y11828) heat shock protein [Arabidopsis thaliana]
Seq. No.
                   224582
                  LIB3166-014-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1370180
BLAST score
                  233
                  2.0e-19
E value
Match length
                  54
                   87
% identity
NCBI Description (Z73939) RAB5B [Lotus japonicus]
                   224583
Seq. No.
                  LIB3166-014-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4008441
BLAST score
                   379
                   1.0e-36
E value
Match length
                   102
```

comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

NCBI Description (AL034488) predicted using Genefinder; cDNA EST yk433c6.3



```
Seq. No.
                  224584
Seq. ID
                  LIB3166-014-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3915847
BLAST score
                  371
E value
                  1.0e-35
Match length
                  81
                  86
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  224585
Seq. ID
                  LIB3166-014-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q3024017
BLAST score
                  430
                  2.0e-42
E value
Match length
                  83
                  98
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
NCBI Description
                   (EIF-4C) >gi 2565421 (AF026804) eukaryotic translation
                  initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.
                  224586
Seq. ID
                  LIB3166-014-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q2662415
BLAST score
                  284
E value
                  2.0e-25
Match length
                  76
% identity
                   61
                 (U97494) metallothionein-like protein [Prunus armeniaca]
NCBI Description
                  224587
Seq. No.
                  LIB3166-014-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063396
BLAST score
                  286
E value
                  1.0e-42
Match length
                  110
% identity
                  82
                 (AB012947) vcCyP [Vicia faba]
NCBI Description
                  224588
Seq. No.
                  LIB3166-014-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244835
BLAST score
                  298
E value
                   4.0e-27
                   91
Match length
% identity
NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
Seq. No.
```

224589

BLASTX

Seq. ID Method

LIB3166-014-P1-K1-E9



```
NCBI GI
                  q3738325
BLAST score
                  403
E value
                  2.0e-39
Match length
                  110
% identity
                  71
                  (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                  thaliana]
                  224590
Seq. No.
                  LIB3166-014-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924777
BLAST score
                  376
E value
                  3.0e-36
Match length
                  130
% identity
NCBI Description
                  (AC002334) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  224591
Seq. ID
                  LIB3166-014-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2662415
BLAST score
                  173
E value
                  2.0e-12
                  56
Match length
% identity
                  54
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]
Seq. No.
                  224592
                  LIB3166-014-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351271
BLAST score
                  331
                  6.0e-31
E value
                  118
Match length
                  62
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
                  >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi 806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
Seq. No.
                  224593
                  LIB3166-014-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1814424
BLAST score
                  582
E value
                  2.0e-60
                  134
Match length
% identity
                  79
NCBI Description (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
                  224594
Seq. No.
```

Seq. ID

LIB3166-014-P1-K1-F8

Method BLASTX NCBI GI g115484



```
555
BLAST score
E value
                   3.0e-57
Match length
                   108
                   59
% identity
                  CALMODULIN 1 >gi 71684 pir MCPZDC calmodulin - carrot
NCBI Description
                   >gi_478632_pir__$22971 calmodulin - trumpet lily
                  >gi_541839_pir__S40301 calmodulin - Red bryony
>gi_2129970_pir__S70768 calmodulin CAM81 - garden petunia
                   >gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota]
                   >gi 19447 emb CAA78301 (Z12839) calmodulin [Lilium
                   longiflorum] >gi_169207 (M80836) calmodulin [Petunia
                   hybrida] >gi_308900 (L18912) calmodulin [Lilium
                   longiflorum] >gi 505154 emb CAA43143 (X60738) Calmodulin
                   [Malus domestica] >gi 535444 (U13882) calmodulin [Pisum
                   sativum] >gi_445602_prf__1909349A calmodulin [Daucus
                   carota]
                   224595
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1709930
BLAST score
                   359
E value
                   2.0e-35
                   94
Match length
                   81
% identity
NCBI Description PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE PRECURSOR (AIR
                   CARBOXYLASE) (AIRC) >gi 629656 pir S43322
                   phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) -
                   moth bean >gi_349159 (L22584) 5-aminoimidazole
                   ribonucleotide carboxylase [Vigna aconitifolia]
                   224596
Seq. No.
                  LIB3166-014-P1-K1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2809251
BLAST score
                   152
                   2.0e-10
E value
Match length
                   34
                   74
% identity
NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]
Seq. No.
                   224597
                   LIB3166-014-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2245087
BLAST score
                   218
                   1.0e-17
E value
Match length
                   86
                   44
% identity
NCBI Description (297343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   224598
Seq. ID
                   LIB3166-014-P1-K1-G5
Method
                   BLASTX
```

g4127456

1.0e-27

303

NCBI GI

E value

BLAST score



Match length 114 % identity 59

NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No. 224599

Seq. ID LIB3166-014-P1-K1-G6

Method BLASTX
NCBI GI g2088651
BLAST score 482
E value 1.0e-48
Match length 123
% identity 70

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 224600

Seq. ID LIB3166-014-P1-K1-G7

Method BLASTX
NCBI GI g2088651
BLAST score 432
E value 8.0e-43
Match length 118
% identity 66

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 224601

Seq. ID LIB3166-014-P1-K1-G9

Method BLASTX
NCBI GI g3212859
BLAST score 505
E value 2.0e-51
Match length 112
% identity 55

NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224602

Seq. ID LIB3166-014-P1-K1-H1

Method BLASTX
NCBI GI g2191136
BLAST score 312
E value 1.0e-28
Match length 110
% identity 60

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase;

coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 224603

Seq. ID LIB3166-014-P1-K1-H10

Method BLASTX
NCBI GI g4510381
BLAST score 219
E value 7.0e-18
Match length 105
% identity 52



```
(AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224604
                  LIB3166-014-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  q2760322
NCBI GI
BLAST score
                  356
                  7.0e-34
E value
                  113
Match length
% identity
                  56
                  (AC002130) F1N21.7 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224605
                  LIB3166-014-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g4049349
NCBI GI
                  363
BLAST score
E value
                  1.0e-34
                  102
Match length
                  71
% identity
                   (AL034567) ubiquinol-cytochrome c reductase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  224606
Seq. No.
                  LIB3166-014-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  g2209332
NCBI GI
BLAST score
                  365
E value
                  7.0e-35
Match length
                  102
                  73
% identity
                  (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis
NCBI Description
                  thaliana] >gi 3927828 (AC005727) chloroplast membrane
                  protein ALBINO3 [Arabidopsis thaliana]
                  224607
Seq. No.
Seq. ID
                  LIB3166-014-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q1237250
                  545
BLAST score
E value
                  5.0e-56
Match length
                  133
% identity
                  77
NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]
                  224608
Seq. No.
                  LIB3166-014-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3269292
BLAST score
                  231
                  3.0e-19
E value
                  64
Match length
% identity
                  66
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
```

224609

LIB3166-015-P1-K1-A2

Seq. No. Seq. ID



Method BLASTX
NCBI GI g3885334
BLAST score 502
E value 7.0e-51
Match length 147
% identity 71

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 224610

Seq. ID LIB3166-015-P1-K1-A4

Method BLASTX
NCBI GI g417103
BLAST score 498
E value 1.0e-50
Match length 111
% identity 94

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa]  $>gi_488577$  (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755 emb\_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 224611

Seq. ID LIB3166-015-P1-K1-A7

Method BLASTX
NCBI GI g4559388
BLAST score 420
E value 3.0e-41
Match length 132
% identity 51

NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No. 224612

Seq. ID LIB3166-015-P1-K1-B1

Method BLASTX
NCBI GI g3759184
BLAST score 351
E value 3.0e-33
Match length 104
% identity 66

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

% identity

NCBI Description



```
Seq. No.
                   224613
Seq. ID
                   LIB3166-015-P1-K1-B2
Method
                  BLASTX
NCBI GI
                   q132944
BLAST score
                   215
E value
                   5.0e-22
Match length
                   92
% identity
                   63
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
                  protein L3 (ARP2) - Arabidopsis thaliana >gi 806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   224614
Seq. ID
                   LIB3166-015-P1-K1-B4
Method
                   BLASTX
NCBI GI
                  q3420049
BLAST score
                   172
E value
                   3.0e-12
Match length
                   131
% identity
                  (AC004680) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   224615
Seq. ID
                  LIB3166-015-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q2191136
BLAST score
                   312
E value
                   1.0e-28
Match length
                   110
                   60
% identity
NCBI Description
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
                  coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
Seq. No.
                   224616
                  LIB3166-015-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953463
BLAST score
                  210
E value
                  1.0e-16
Match length
                   60
% identity
                   60
NCBI Description
                 (AC002328) F20N2.8 [Arabidopsis thaliana]
                  224617
Seq. No.
                  LIB3166-015-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g728906
BLAST score
                  330
E value
                  8.0e-31
Match length
                  126
                  55
```

>gi\_1077722\_pir\_\_S50669 hypothetical protein YER166w yeast (Saccharomyces cerevisiae) >gi 603407 (U18922)

PROBABLE CALCIUM-TRANSPORTING ATPASE 5